



1/64

1 ATGTGGAAATGGATACTGACACATTGTGCCTCAGCCTTTCCCCACCTGCCCCGGCTGCTGC 60
-----+-----+-----+-----+-----+-----+
TACACCTTTACCTATGACTGTGTAACACGGAGTCGGAAGGGGTGGACGGGGCCGACGACG
M W K W I L T H C A S A F P H L P G C C
61 TGCTGCTGCTTTTTGTTGCTGTTCTTGGTGTCTTCCGTCCCTGTCACCTGCCAAGCCCTT 120
-----+-----+-----+-----+-----+-----+
ACGACGACGAAAAACAACGACAAGAACCACAGAAGGCAGGGACAGTGGACGGTTCGGGAA
C C C F L L L F L V S S V P V T C Q A L
121 GGTCAGGACATGGTGTCAACAGAGGCCACCAACTCTTCTCCTCCTCCTCCTCCTCCT 180
-----+-----+-----+-----+-----+-----+
CCAGTCCTGTACCACAGTGGTCTCCGGTGGTTGAGAAGAAGGAGGAGGAAGAGGAGAGGA
G Q D M V S P E A T N S S S S S F S S P
181 TCCAGCGCGGGAAGGCATGTgCGGAGCTACAATCACCTTCAAGGAGATGTCCGCTGGAGA 240
-----+-----+-----+-----+-----+-----+
AGGTGCGGCCCTTCCGTACAcGCCTCGATGTTAGTGGAAGTTCCTCTACAGGCGACCTCT
S S A G R H V R S Y N H L Q G D V R W R

MATCH WITH FIG. 1B

FIG.1A



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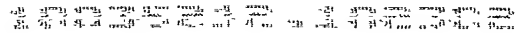
2/64

MATCH WITH FIG. 1A

241 AAGCTATTCTCTTTCACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGGTCAGCGGG 300
-----+-----+-----+-----+-----+-----+
TTCGATAAGAGAAAGTGGTTCATGAAAGAGTTCTAACTCTTCTTGGCCTTCCAGTCGCC
K L F S F T K Y F L K I E K N G K V S G
301 ACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT 360
-----+-----+-----+-----+-----+-----+
TGGTTCTTCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA
T K K E N C P Y S I L E I T S V E I G V
361 GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAACTC 420
-----+-----+-----+-----+-----+-----+
CAACGGCAGTTTCGGTAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAG
V A V K A I N S N Y Y L A M N K K G K L
421 TATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA 480
-----+-----+-----+-----+-----+-----+
ATACCGAGTTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT
Y G S K E F N N D C K L K E R I E E N G

MATCH WITH FIG. 1C

FIG.1B



MATCH WITH FIG. 1B

481 TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG 540
-----+-----+-----+-----+-----+-----+
ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATACACCGTAAC

Y N T Y A S F N W Q H N G R Q M Y V A L

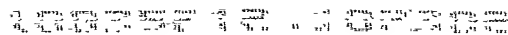
AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC
541 -----+-----+-----+-----+-----+-----+ 600
TTACCTTTTCCTCGAGGTTCCCTCTCCTGTCTTTTGTGCTTCCTTTTTGTGGAGACGAGTG

N G K G A P R R G Q K T R R K N T S A H

TTTCTTCCAATGGTGGTACACTCATAG
601 -----+-----+----- 627
AAAGAAGGTTACCACCATGTGAGTATC

F L P M V V H S *

FIG. 1 C



i

	51				100
FGF4	AELERRWESL	VALSLARLPV	AA..QPKEAA	VQSGAGDY..	...LLGIKRL
FGF6	S...RGWGTL	LSRSRAGLAG	EI.....AG	VNWESG.Y..	...LVGIKRQ
FGF5	SSSRQSSSSA	MSSSSASSSP	AASLGSQGS	LEQSSFQW..	...SPSGRRT
FGF1MAEG	EITTTALTE	KFN...LPPGN..	...YK...KP
FGF2MAAG	SITTLPALPE	DGGSGAFPPGH..	...FK...DP
FGF9	FGNVPVLPVD	SPVLLSDHLG	QSEAGGLPRG	PAVTDLDH..	...LKGILRR
FGF7	LACNDMTPEQ	M...ATNVNCSSPE	RHTRSYDY..	...MEGGDIR
KGF2	VTCQALGQDM	VSPEATNSSS	SSFSSPSSAG	RHVRSYNH..	...LQ.GDVR
FGF3	PGWPAAGPGARLRRDAG	GRGGVYEH..	...L.GGAPR
FGF8	FGQSRAGKN	FTNPAPNYPE	EGSKEQRDSV	LPKVTQRHVR	EQSLVTDOLS

FIG. 2A



101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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MATCH WITH FIG. 2A

	101		150
FGF4	RRL.....YC	NVGIGFHLQA	LPDGRIGGAH ADT.RDSLLE LSPVERGV.V
FGF6	RRL.....YC	NVGIGFHLQV	LPDGRISGTH EEN.PYSLLE ISTVERGV.V
FGF5	GSL.....YC	RVGIGFHLQI	YPDGKVNGSH EAN.MLSVLE IFAVSQGI.V
FGF1	KLL.....YC	SNG.GHFLRI	LPDGTVDGTR DRSDQHIQLQ LSAESVGE.V
FGF2	KRL.....YC	KNG.GFFLRI	HPDGRVDGVR EKSDPHIKLQ LQAEERGV.V
FGF9	RQL.....YC	R.T.GFHLEI	FPNGTIQGTR KDHSRFGILE FISIAVGL.V
FGF7	VRR.....LF	CRT.QWYLRI	DKRGKVKGTO EMKNNYNIME IRTVAVGI.V
KGF2	WRK.....LF	SFT.KYFLKI	EKNGKVSGTK KENCYPYSILE ITSVEIGV.V
FGF3	RRK.....LY	CAT.KYHLQL	HPSGRVNGSL .ENSAYSILE ITAVEVGI.V
FGF8	RRLIRTYQLY	SRTSGKHVQV	LANKRINAMA EDGDPPFAKLI VETDTFGSRV

	151		200
FGF4	SIFGVASRFF	VAMSSKGKLY	G.SPFFTDEC TFKEILLPNN YNAYESYKYP
FGF6	SLFGVRSALF	VAMNSKGRLY	A.TPSFQEEC KFRETLLPNN YNAYESDLYQ
FGF5	GIRGVFSNKF	LAMSKKGKLY	A.SAKFTDDC KFRERFQENS YNTYASAIHR
FGF1	YIKSTETGQY	LAMDTDGLLY	G.SQTPNEEC LFLERLEENH YNTYISKKH.
FGF2	SIKGVCANRY	LAMKEDGRLL	A.SKCVTDEC FFFERLESNN YNTYRSRKY.
FGF9	SIRGVDSGLY	LGMNEKGELY	G.SEKLTQEC VFREQFEENW YNTYSSNLYK
FGF7	AIKGVESEFY	LAMNKEGKLY	A.KKECNEDC NFKELILENH YNTYAS....
KGF2	AVKAINSNY	LAMNKKGKLY	G.SKEFNDC KLKERIEENG YNTYAS....
FGF3	AIRGLFSGRY	LAMNKRGRLY	A.SEHYSAEC EFVERIHELG YNTYASRLYR
FGF8	RVRGAETGLY	ICMNNKGKLY	AKSNGKGKDC VFTEIVLENN YTAQNQAKY.

MATCH WITH FIG. 2C

FIG. 2B



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MATCH WITH FIG. 2B

	201	250
FGF4 GM..... FI	ALSKNGKTKK G..NRVSPTM KVTHFLPRL.
FGF6 GT..... YI	ALSKYGRVKR G..SKVSPIM TVTHFLPRI.
FGF5 TEKTGREWYV	ALNKRKGAKR GCSPRVKPQH ISTHFLPRFK
FGF1AEKNWFV	GLKKNNGSCKR G..PRTHYGQ KAILFLPLPV
FGF2T..SWYV	ALKRTGQYKL G..SKTGPGQ KAILFLPMSA
FGF9	HV..... ..DTGRRYYV	ALNKDGTPRE G..TRTKRHQ KFTHFLPRPV
FGF7 AKW THNGGEM.FV	ALNQKGIPVR G..KKTKKEQ KTAHFLPMAI
KGF2 FNW QHNGRQM.YV	ALNGKGAPRR G..QKTRRNK TSAHFLPMVV
FGF3	TVSSTPGARR QPSAERLWYV	SVNGKGRPRR G..FKTRRTQ KSSLFLPRVL
FGF8EGWYM	AFTRKGRPRK G..SKTRQHQ REVHFMKRLP

	251	300
FGF4
FGF6
FGF5	QSEQPELSFT VTVPEKKNPP	SPIKSKIPLS APRKNTNSVK YRLKFRFG..
FGF1	SSD.....
FGF2	KS.....
FGF9	DPDKVPELYK DILSQS....
FGF7	T.....
KGF2	HS.....
FGF3	DHRDHEMVRQ LQSGLP RPPG	KGVP RRRRRQ KQSPDNLEPS HVQASRLGSQ
FGF8	RGHHTTEQSL RFEFLNYPPF	TRSLRGSQRT WAPEPR....

MATCH WITH FIG. 2D

FIG. 2C

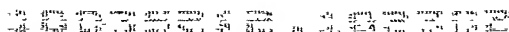


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MATCH WITH FIG. 2C

	301
FGF4
FGF6
FGF5
FGF1
FGF2
FGF9
FGF7
KGF2
FGF3	LEASAH
FGF8

FIG.2D

[illegible][illegible][illegible]



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AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr	1123
GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg	1171
AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	1216
TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG	1276
GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC	1336
TAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCACTG CTGACATATG ATGTTCTTTT	1396
AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT	1456
ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTGTGTGT TGTGTCAAG TTTTGTGTTT	1516
TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG	1576
GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT	1636
GAATCAATGA ACAGTAATAC GTGCAAGCAT TTACTGGAAA GCACTTGGGT CATATCATAT	1696
GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAAATA	1756
TAAACATGTT AGTGTGAAAC TGTCTAACA ATACAAATAG TATGGTATGC TTGTGCATTC	1816
TGCCTTCATC CCTTTCTATT TCTTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT	1876
TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG	1936
CACACCACAT GCATGTTTAC GACAAAGTGT TTTTAAAACT TGGCGAACAC TTCAAAAATA	1996
GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA	2056
CTTCTGCAGT AATAACCATC AACATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG	2116
AGATGTCTGC TATCATTTGA AAACATATAT TACTCTGAG GCTTCCTGTC TCAAGAAATA	2176
GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA	2236
AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT	2296
TTCTTGCCAA ATGTCATGGC GGTAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA	2356
TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAGAAT TTGGTATGAA GCGCAACTCT	2416

FIG.3B



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CCCAGGGGCT TAACTGAGC AATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA	2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT ACAAACCAA ATAAACTTG TTTTCTGTAA	2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCATT TTGTTAGAGC	2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT	2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTTA AAAATGTAGA AAAATACTAT	2716
TTGTTCTAAA TACTTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT	2776
CATATTTCTT GTTTTGAAAA AGCATTTTAT TGTTTGGACA CAGTATTTTG GTACAAAAAA	2836
AAAGACTCAC TAAATGTGTC TTAATAAAGT TTAACCTTTG GAAATGCTGG CGTTCGTGA	2896
TTCTCCAACA AACTTATTTG TGTCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT	2956
TTAAAAATTG CTTTATTAAG AAATTTTTTG TATAATCCCA TAAAAGGTCA TATTTTTCCC	3016
ATTCTTCAAA AAAACTGTAT TTCAGAAGAA ACACATTGGA GGCAGTGTCT TTTGGCTTAT	3076
AGTTTAAATT GCATTCATC ATACTTTGCT TCCAAGTGC TTTTGGCAA ATGAGATTAT	3136
AAAAATGTTT AATTTTTGTG GTTGAATCT GGATGTTAAA ATTTAATTGG TAACTCAGTC	3196
TGTGAGCTAT AATGTAATGC ATTCCTATCC AAAGTAGGTA TCTTTTTTTC CTTTATGTTG	3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTTG	3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAAA CAGGGCACAA ACTGGATTCT	3376
TATTTACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG	3436
TACTCAAGAC ACTAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT	3496
AGAAAACATC TCCCCTGTCT CTCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG	3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTTGGGAGA CTGTGGGAAG ATGGCTTGAG	3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA	3676
AAACAAAACA AATGTAGCCA TCGTGGTGG CATATACCTG TGGTCCCAAC TACTCAGGAG	3736
GCTGAAACGG AAGGATCTCT TGGGCCCCAG GAGTTTGAGG CTGCAGTGAG CTATAATCTT	3796
GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA	3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA	3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA	3976
GATTGTTTGG TAAGGAGTAA TGACATTCTC TTGCATTAA AAGTGGCATA TTTGCTTGAA	4036

FIG.3C



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ATGGAATAG AATTCTGGTC CCTTTTGCAA CTA CTGAGA AAAAAAAAAAG CAGTTTCAGC 4096
CCTGAATGTT GTAGATTGA AAAAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA 4156
TTCGCCCTAT AGTGAGTCGT A 4177

FIG.3D



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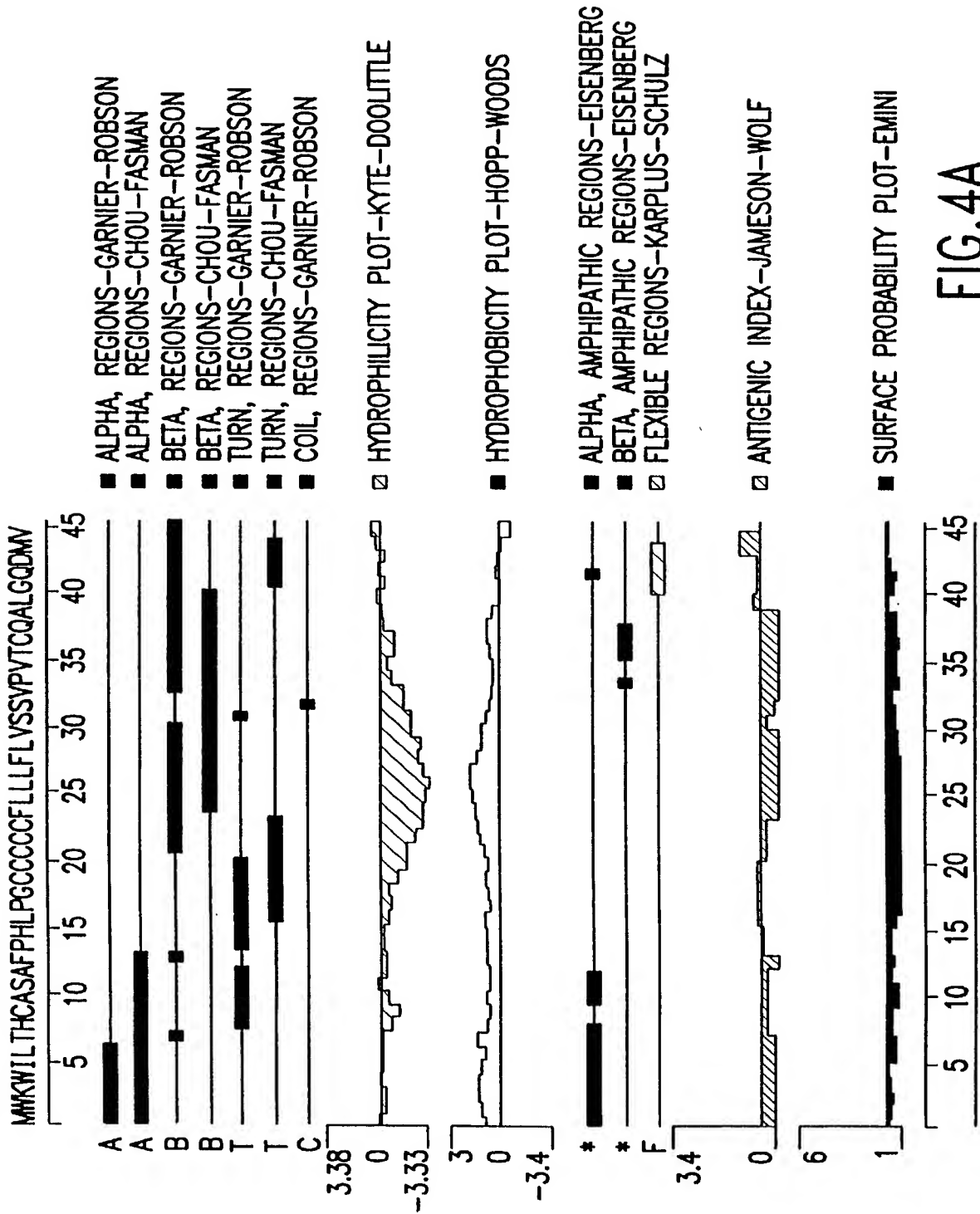
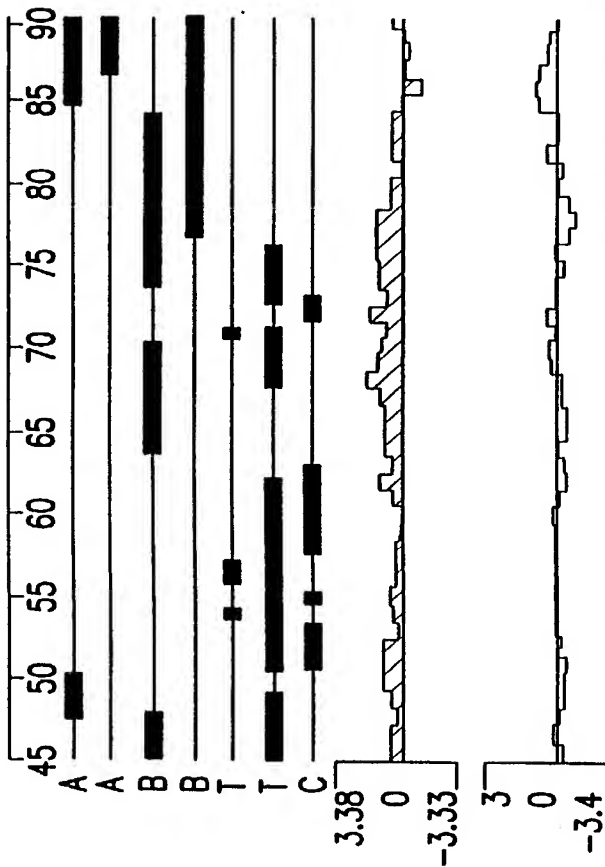


FIG.4A



SPEATNSSSFSSPSSAGRIHRSYNIHLQGDVRMRKLFSTKYFL



- ALPHA, REGIONS-GARNIER-ROBSON
- ALPHA, REGIONS-CHOU-FASMAN
- BETA, REGIONS-GARNIER-ROBSON
- BETA, REGIONS-CHOU-FASMAN
- TURN, REGIONS-GARNIER-ROBSON
- TURN, REGIONS-CHOU-FASMAN
- COIL, REGIONS-GARNIER-ROBSON

□ HYDROPHILICITY PLOT-KYTE-DOOLITTLE

□ HYDROPHOBICITY PLOT-HOPP-WOODS



- ALPHA, AMPHIPATHIC REGIONS-EISENBERG
- BETA, AMPHIPATHIC REGIONS-EISENBERG
- FLEXIBLE REGIONS-KARPLUS-SCHULZ

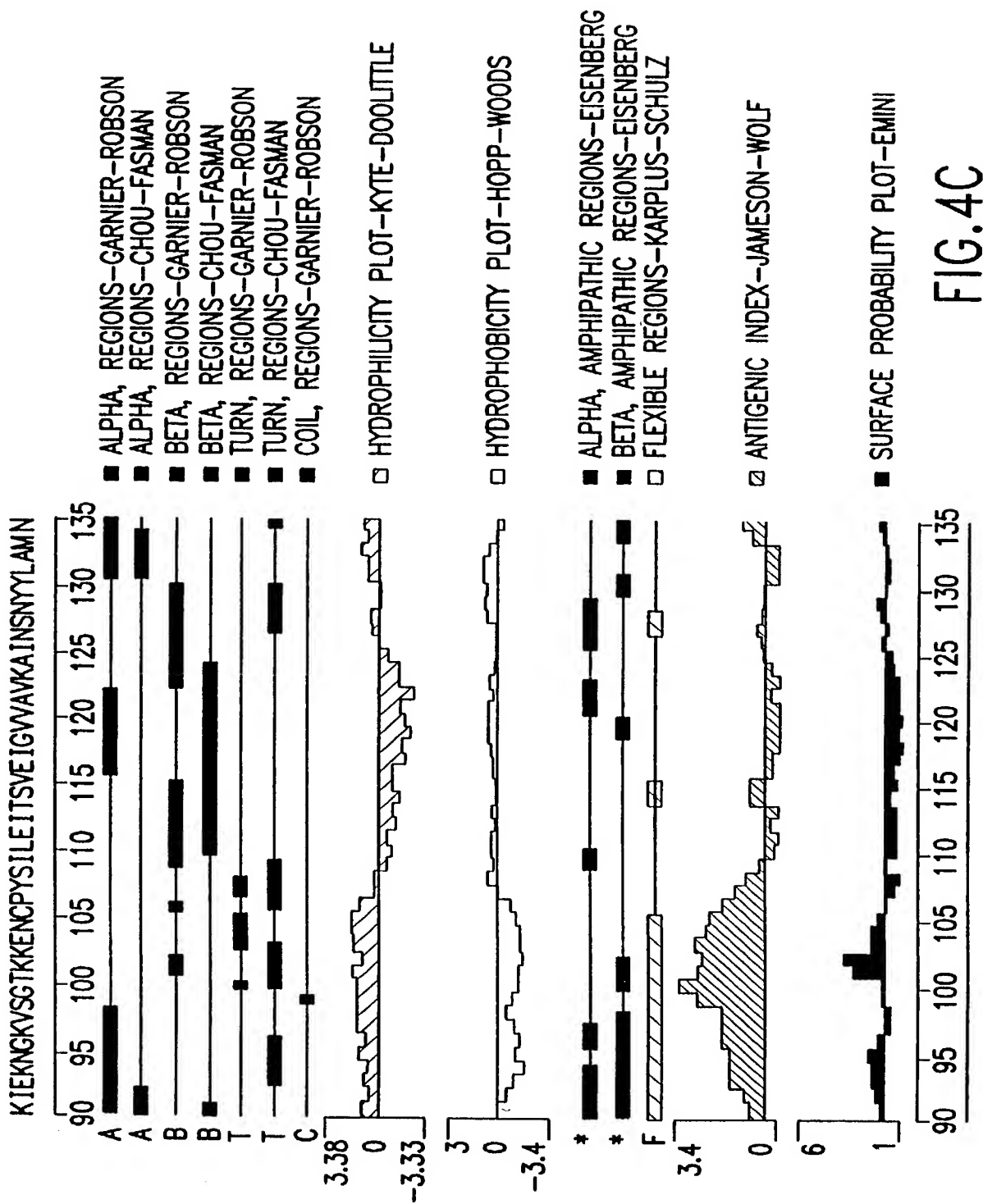
□ ANTIGENIC INDEX-JAMESON-WOLF

■ SURFACE PROBABILITY PLOT-EMINI

FIG.4B



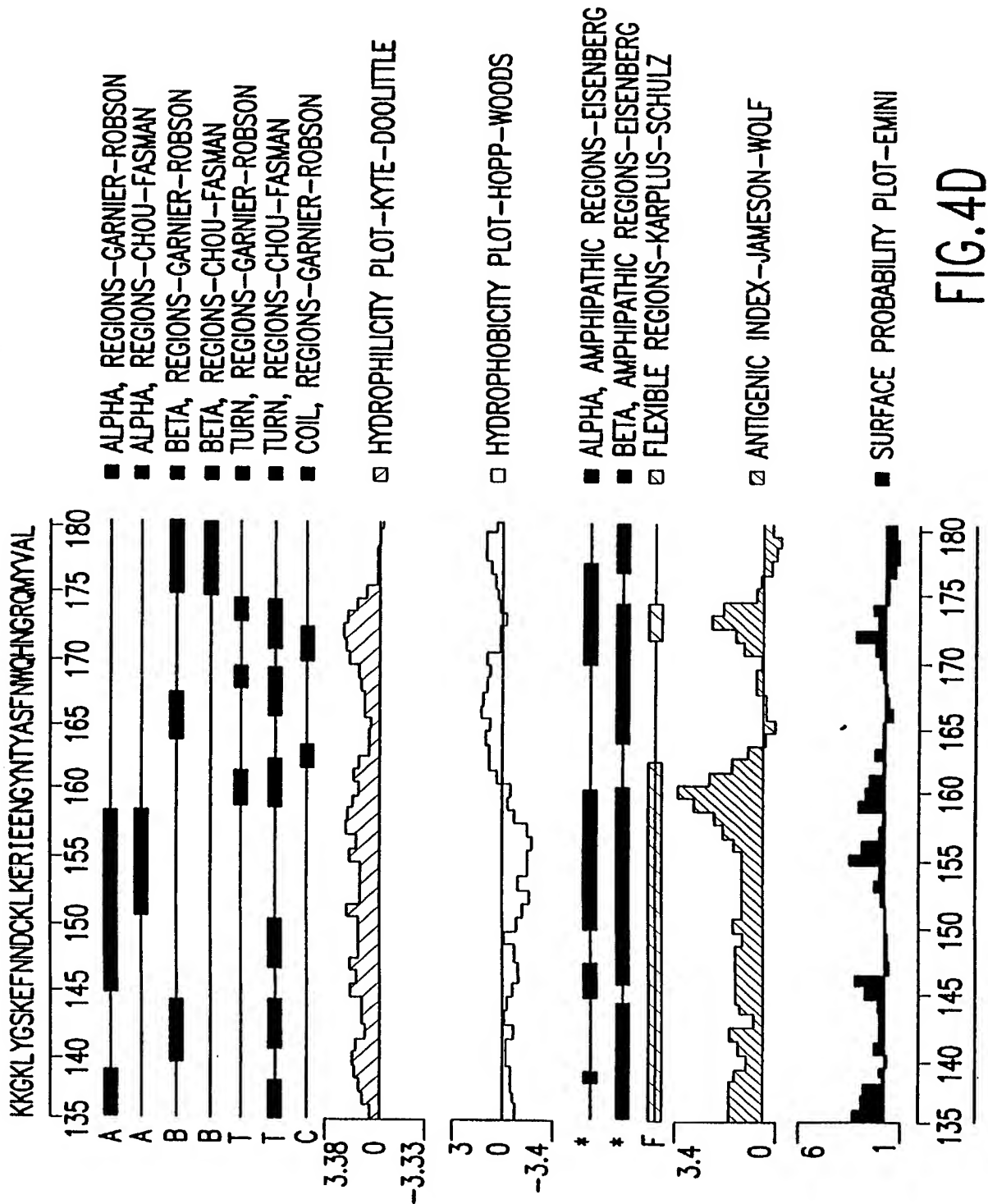
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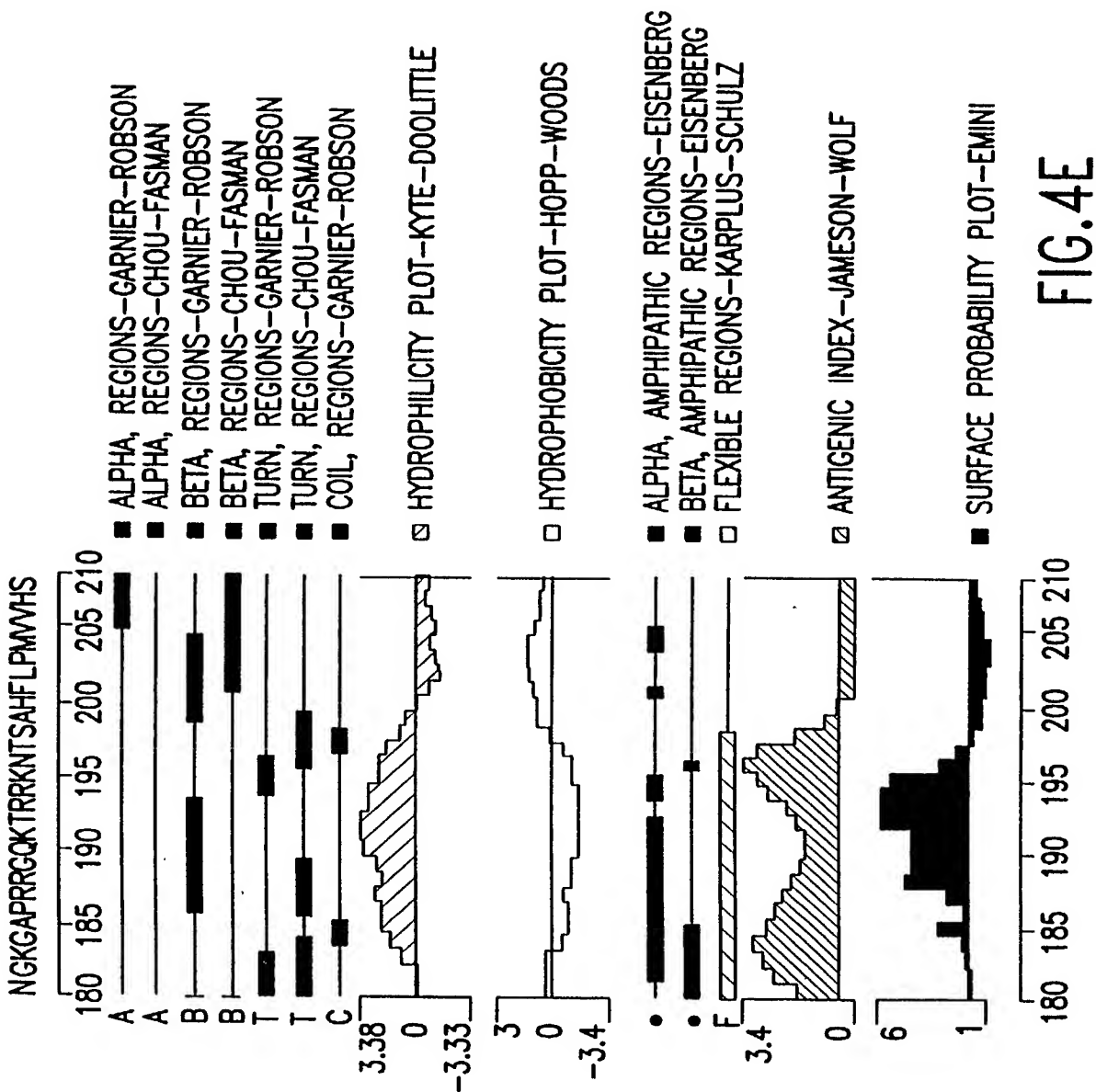


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Patent & Trademark Office, QIP, New Delhi, India. The date of filing of the patent application is 17/06/2002. The date of grant of the patent is 23/10/2002. The patent number is 17/64.

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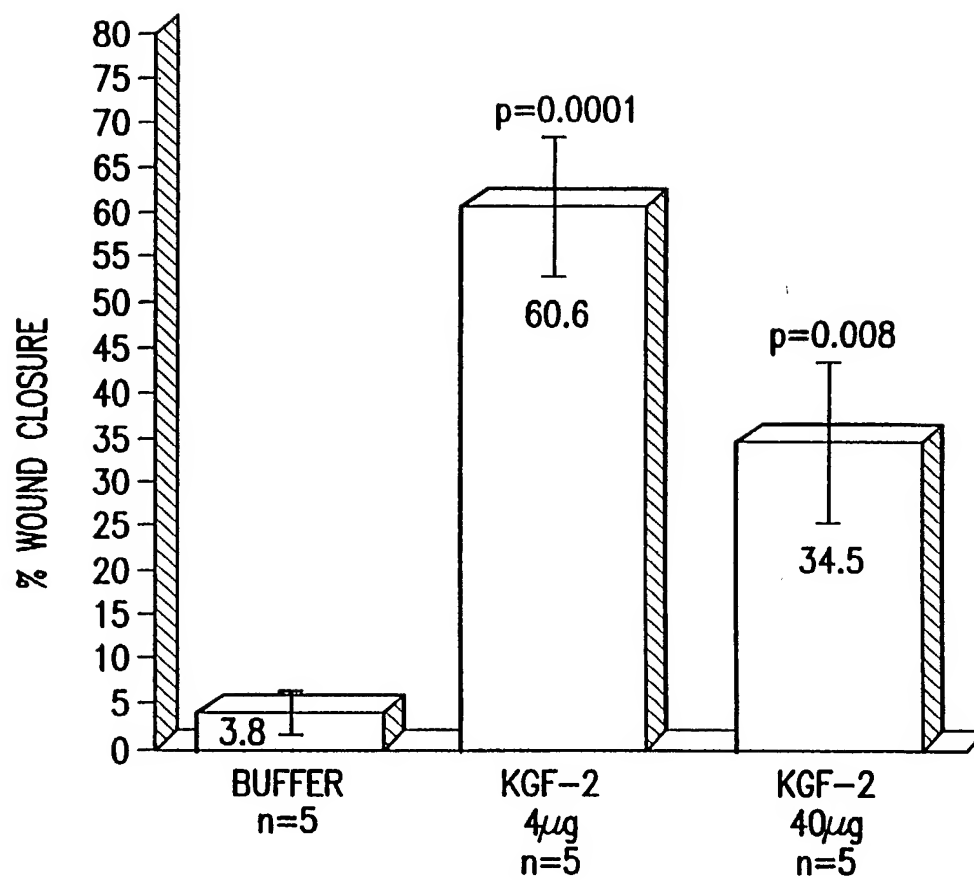


FIG.5



01/01/2002 10:00:00 AM

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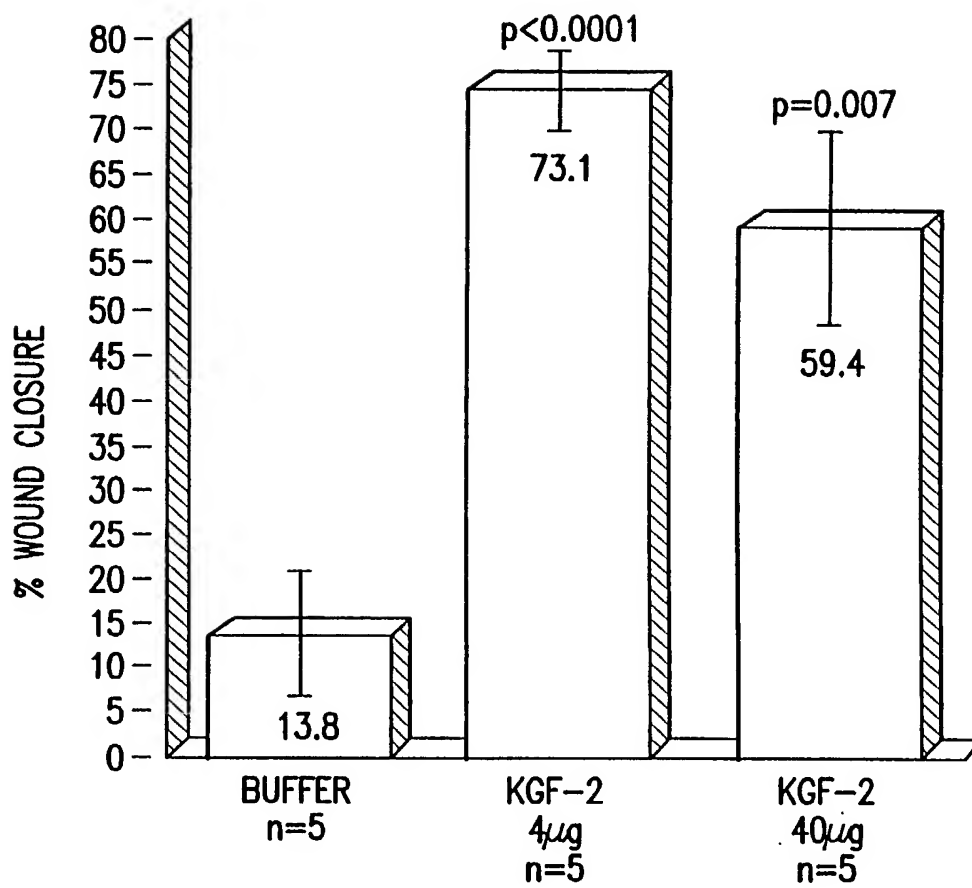


FIG.6



FIG. 7 is a line graph showing the wound measure area (sq. mm) over time (days postwounding) for three groups: KGF-2 40µg n=5, KGF-2 4µg n=5, and VEHICLE n=5. The y-axis ranges from 10 to 100 sq. mm, and the x-axis ranges from 1 to 8 days postwounding. The VEHICLE group shows the highest wound measure area, while the KGF-2 groups show a significant decrease in wound measure area over time, with the 40µg group showing the most rapid and significant reduction.

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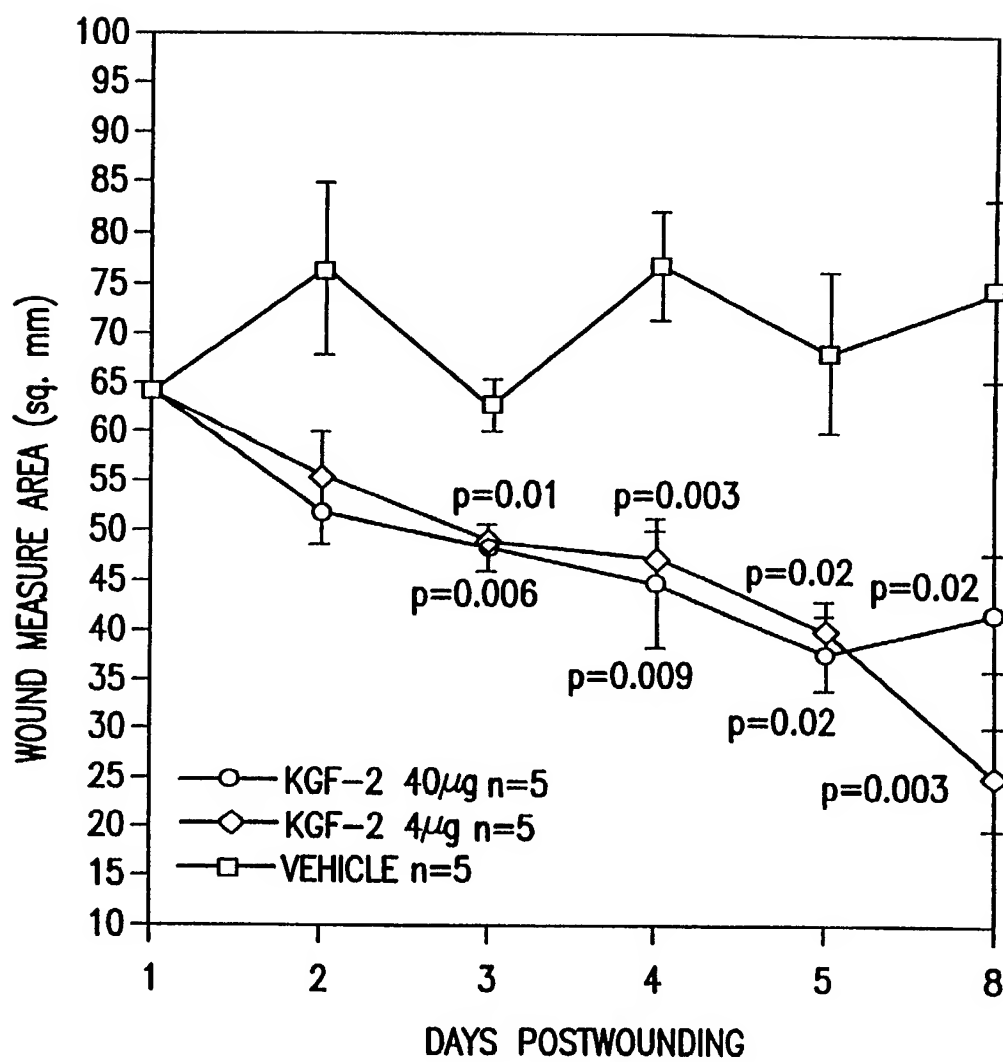


FIG.7



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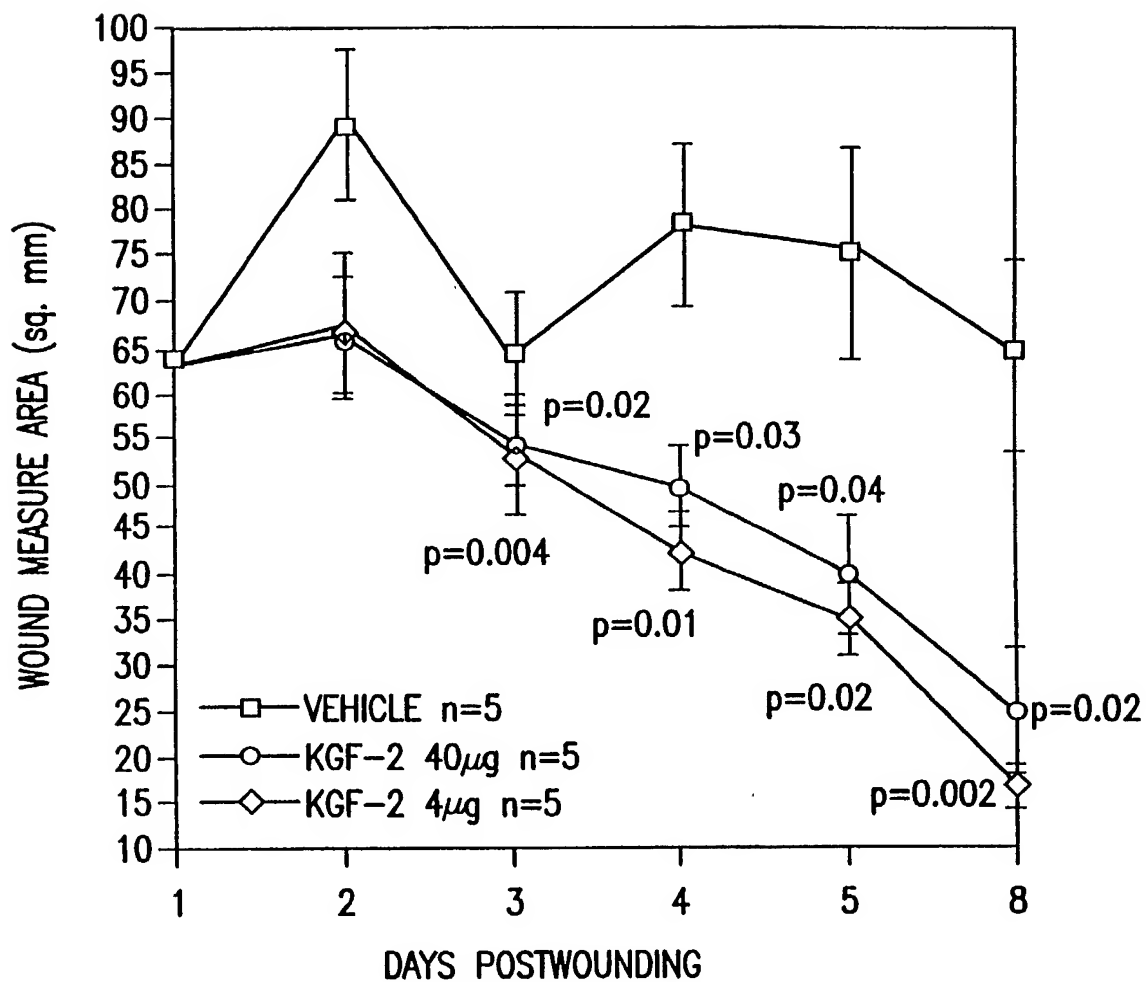
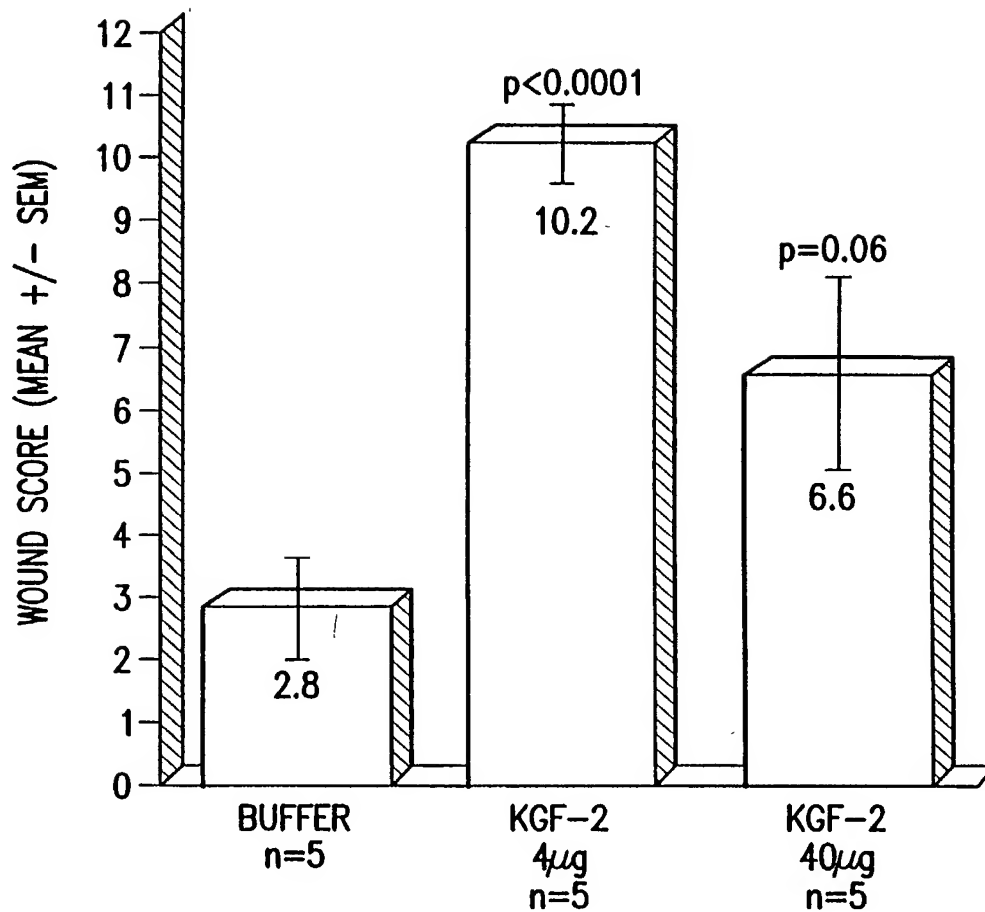


FIG.8



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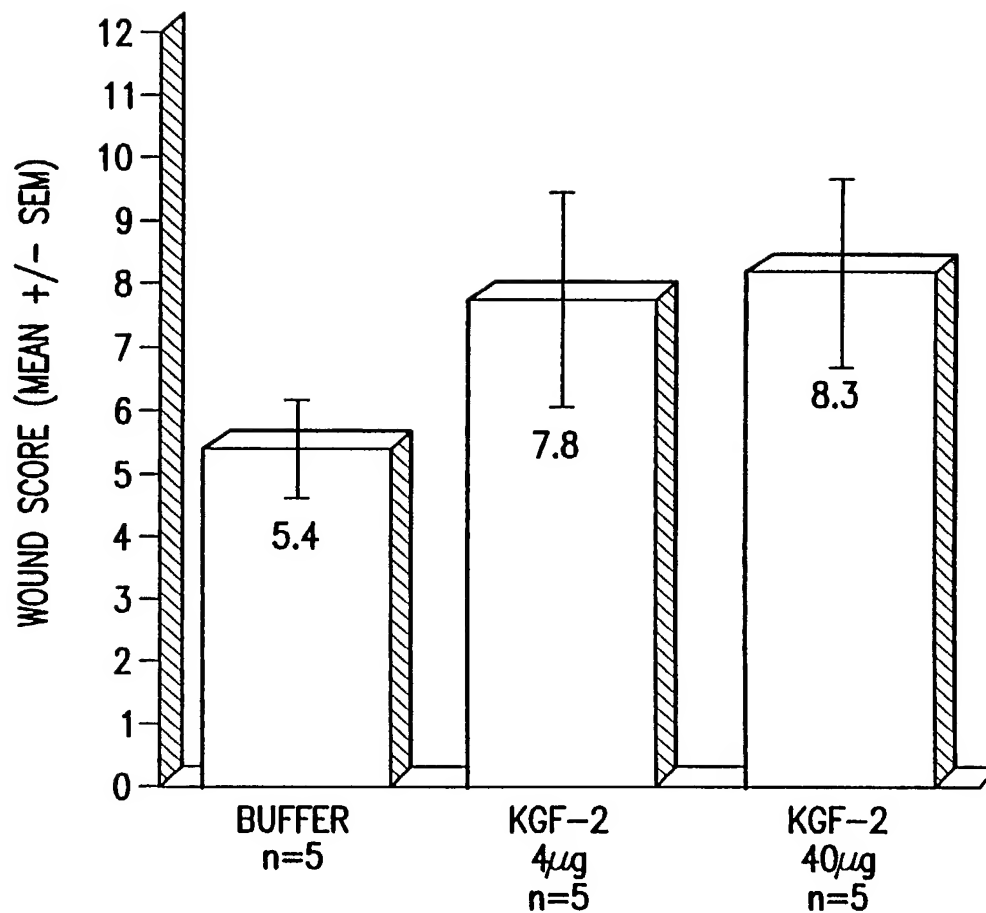


1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.9



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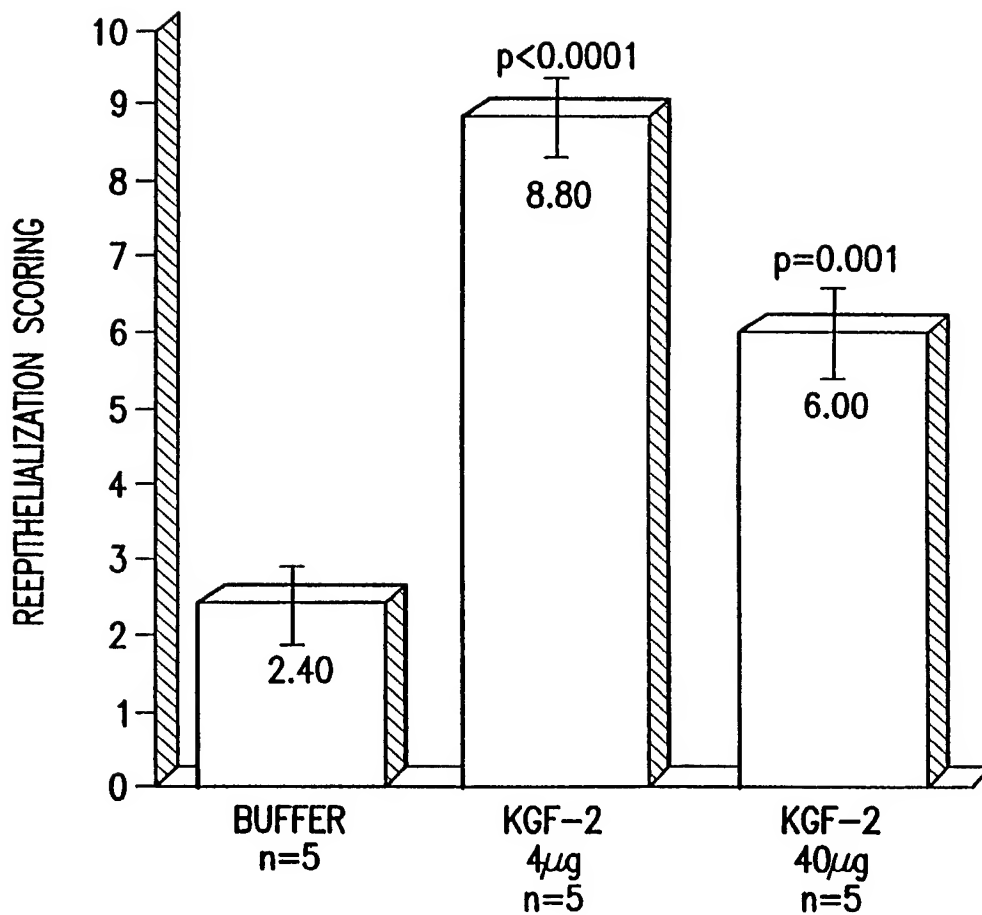


1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES
7-9 GRANULATION TISSUE, CELLS, FIBROBLASTS, NEW EPITHELIUM
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.10



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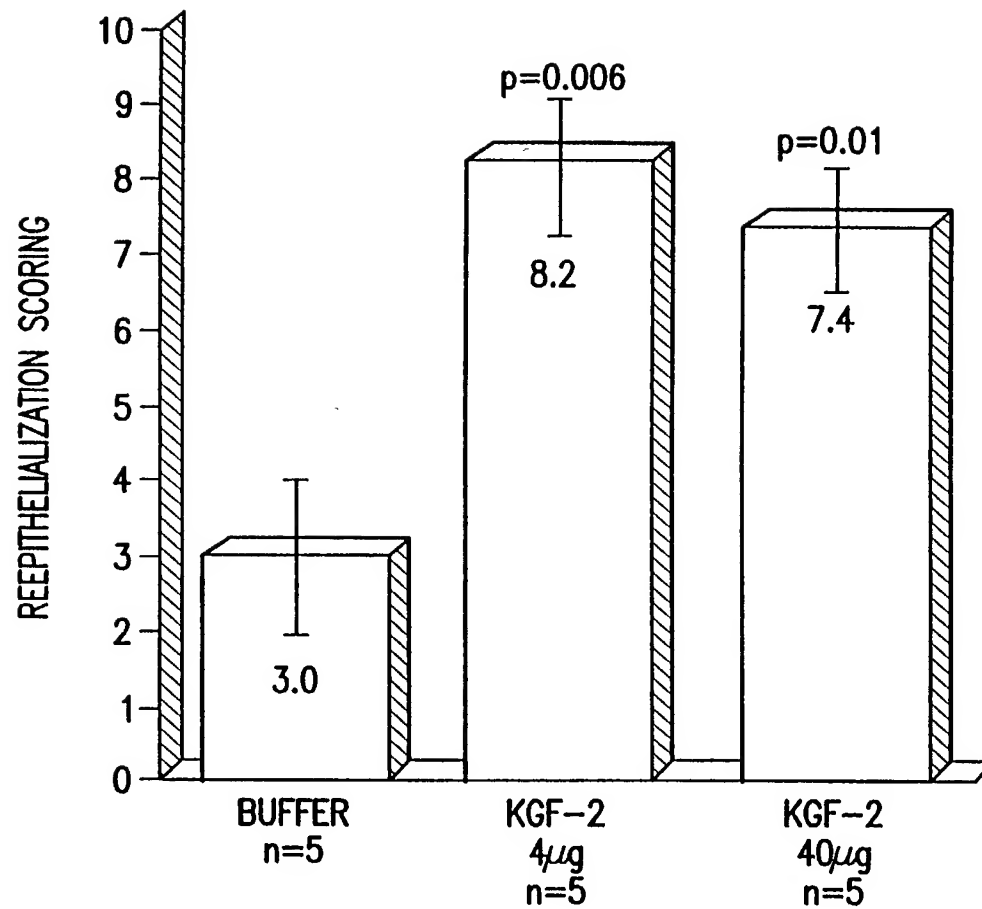
ANTI-CYTOKERATIN IMMUNOSTAINING
0-NO CLOSURE
5-SLIGHT TO MODERATE CLOSURE
10-COMPLETE CLOSURE

FIG.11



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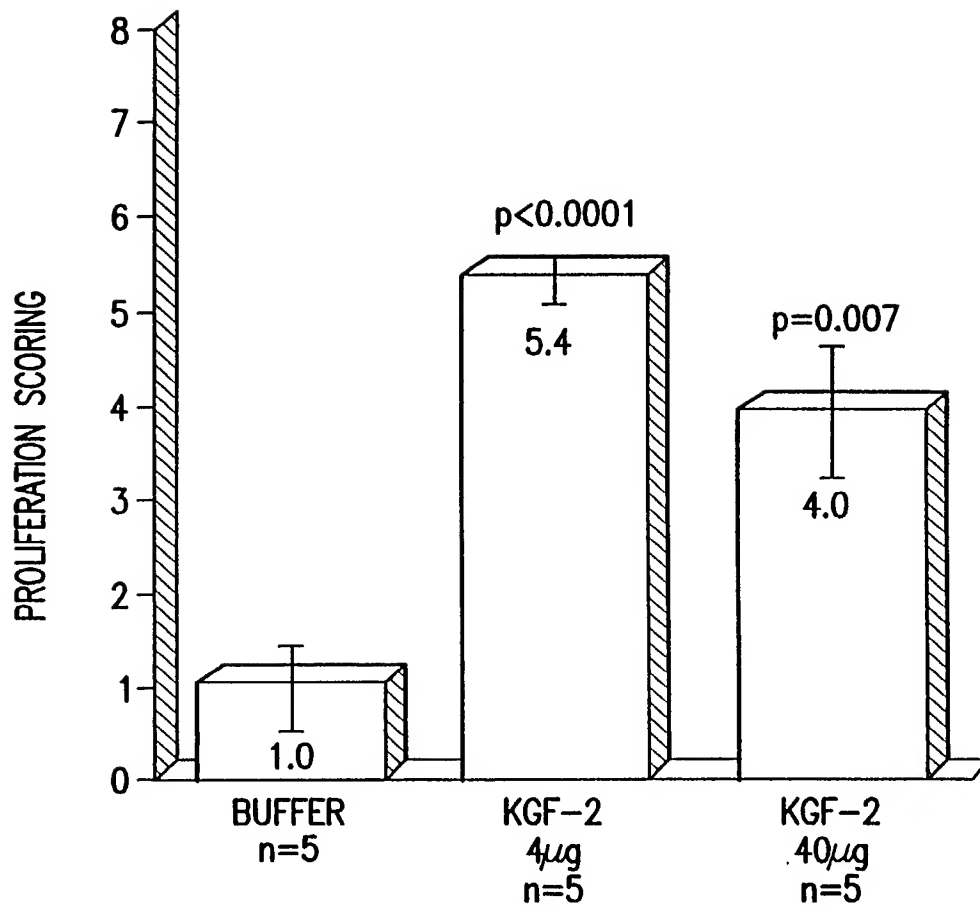
ANTI-CYTOKERATIN IMMUNOSTAINING
0-NO CLOSURE
5-SLIGHT TO MODERATE CLOSURE
10-COMPLETE CLOSURE

FIG.12



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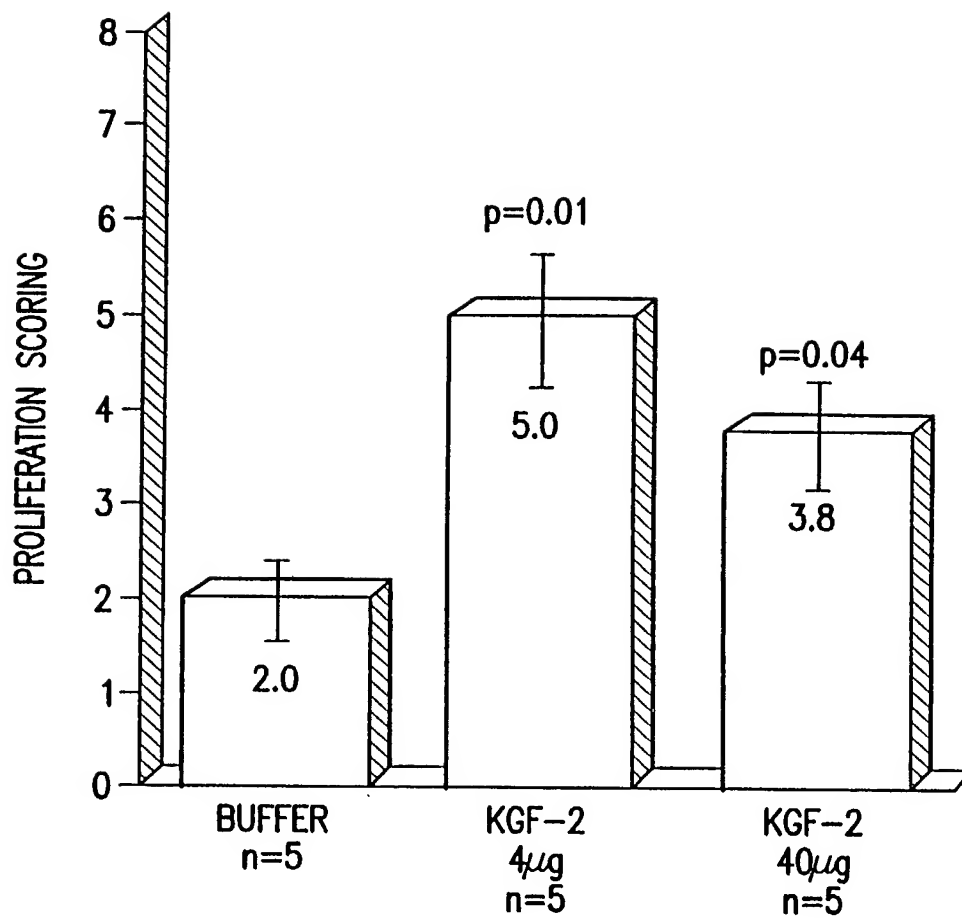


PCNA SCORING
0-2 SLIGHT PROLIFERATION
3-5 MODERATE PROLIFERATION
6-8 INTENSE PROLIFERATION

FIG.13



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PCNA SCORING
0-2 SLIGHT PROLIFERATION
3-5 MODERATE PROLIFERATION
6-8 INTENSE PROLIFERATION

FIG.14



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ATGAGAGGATCGCATCACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC
AGGACATGGTTTCTCCGGAAGCTACCAACTCTTCTCTTCTCTTCTCTTCCC
CGTCTTCCGCTGGTCGTCACGTTGTTCTTACAACCACCTGCAGGGTGACGTTCT
GTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCTGAAAATCGAAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAAGTCCCGTACAGCATCCTG
GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAG
CAACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAAG
AATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT
ACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGAaTGGAAAAGGAGCTCCAaGGAGAGGACAGAAAACACGAAG
GAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MRGSHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD
VRWRKLFSTKYFLKIEKNGKVS GTKKENC PYSILEITSVEIGVVAVKAINSN
YYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS

kgf-2 synthetic cys37 Bam HI
AAAGGATCCTGCCAGGCTCTGGGTCAGGACATG

FIG.15



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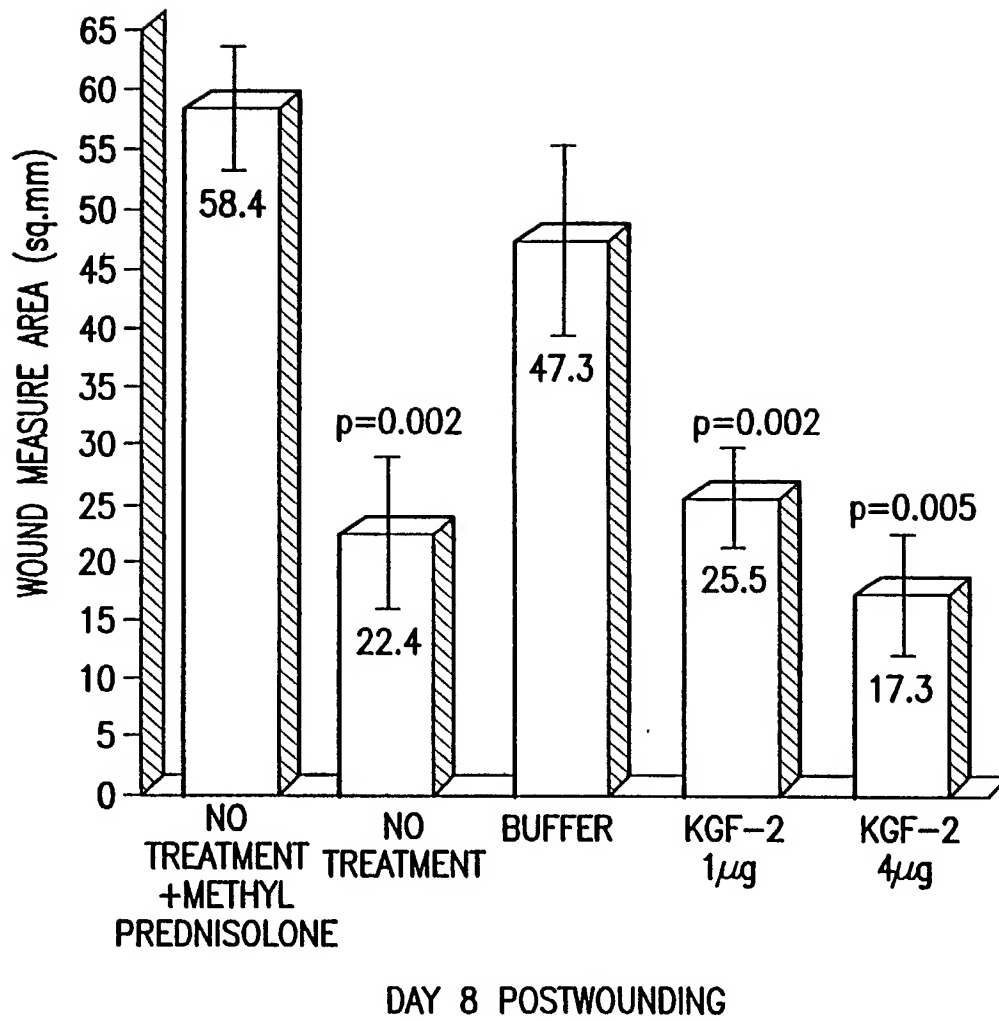
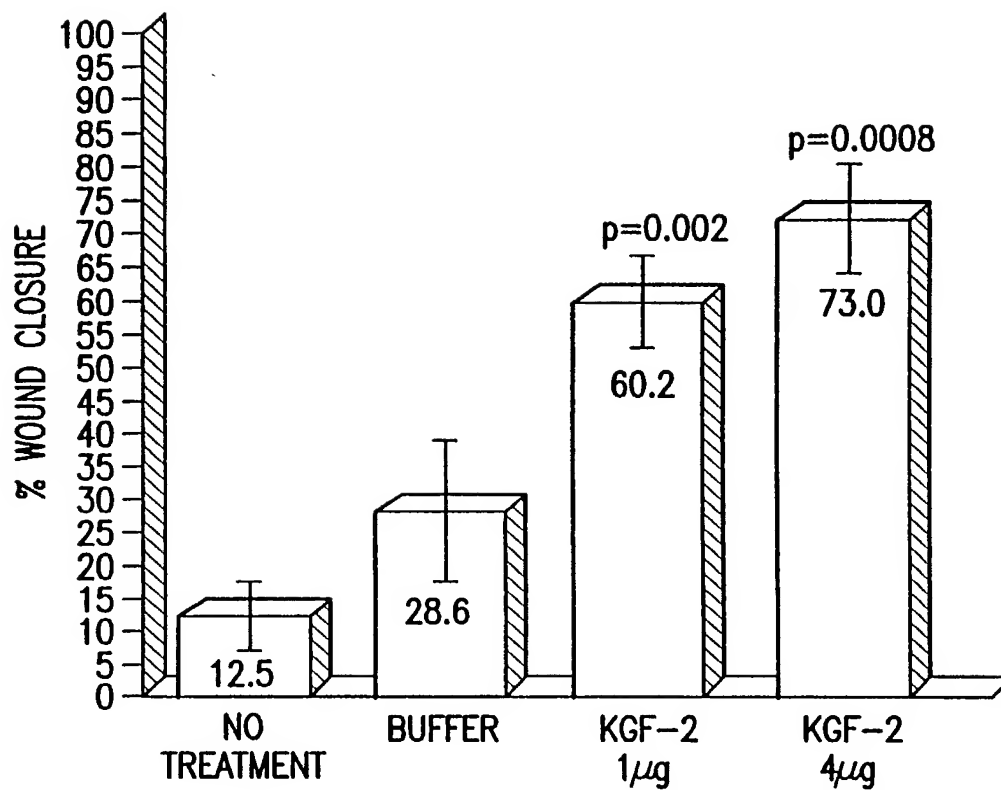


FIG.16



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GLUCOCORTICOID TREATED ANIMALS

FIG.17



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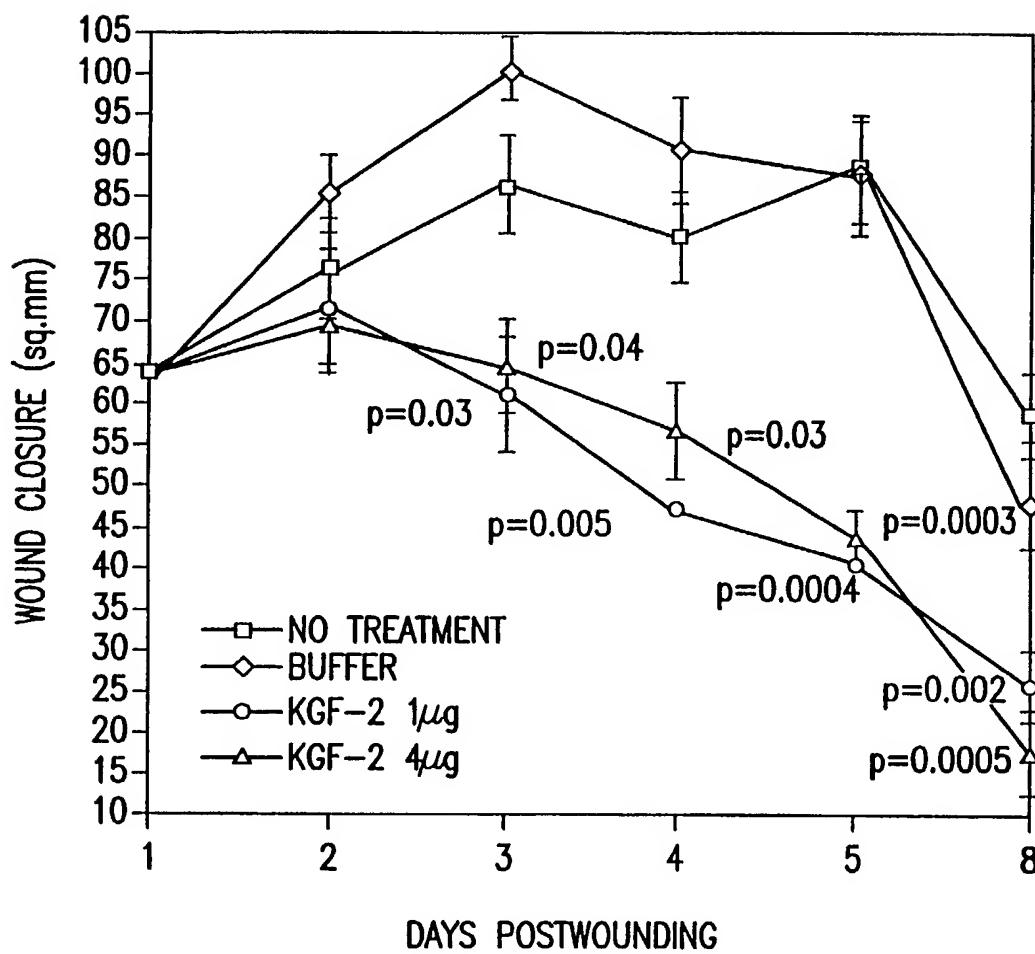


FIG.18



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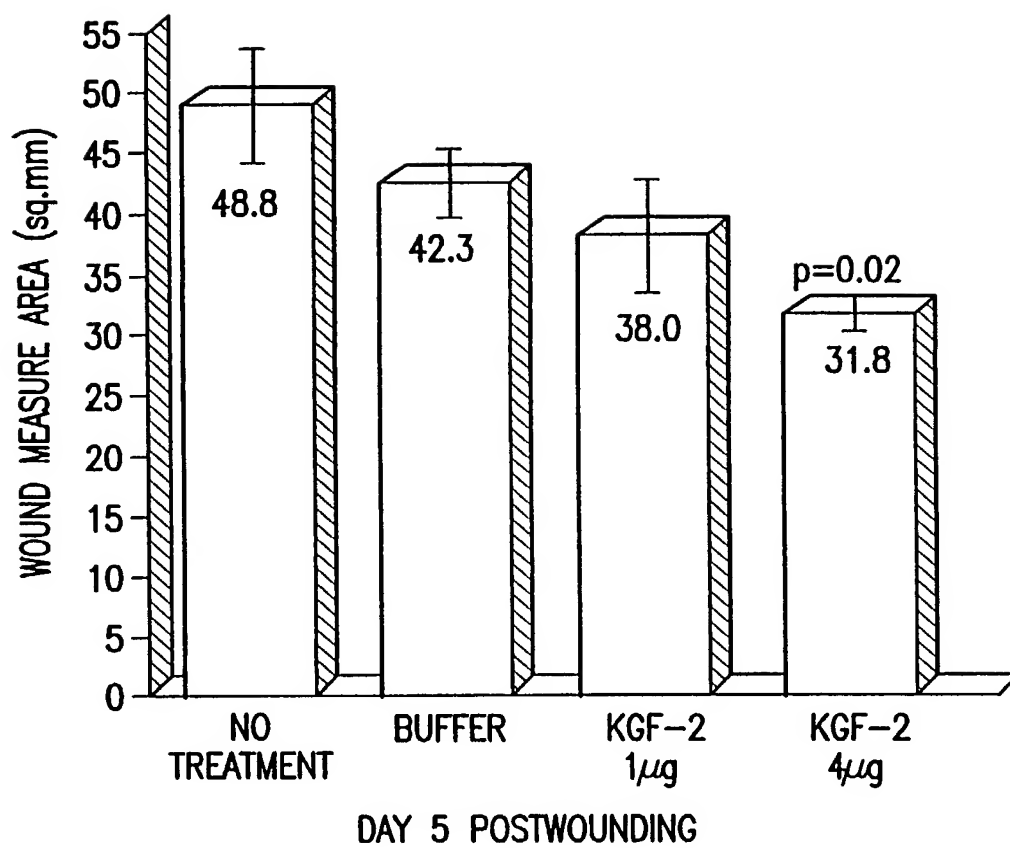
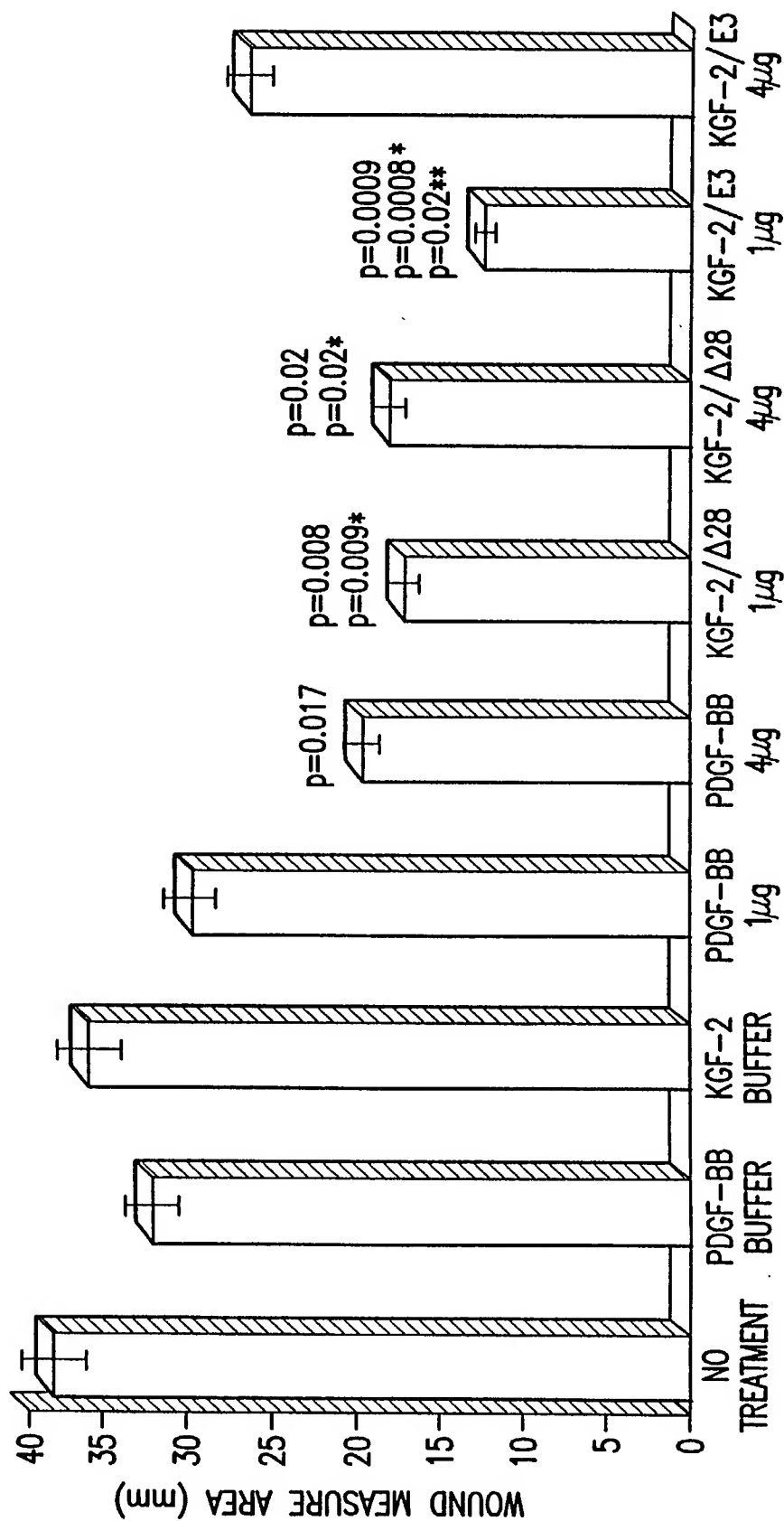


FIG.19A



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DAY 10 POSTWOUNDING

FIG.19B



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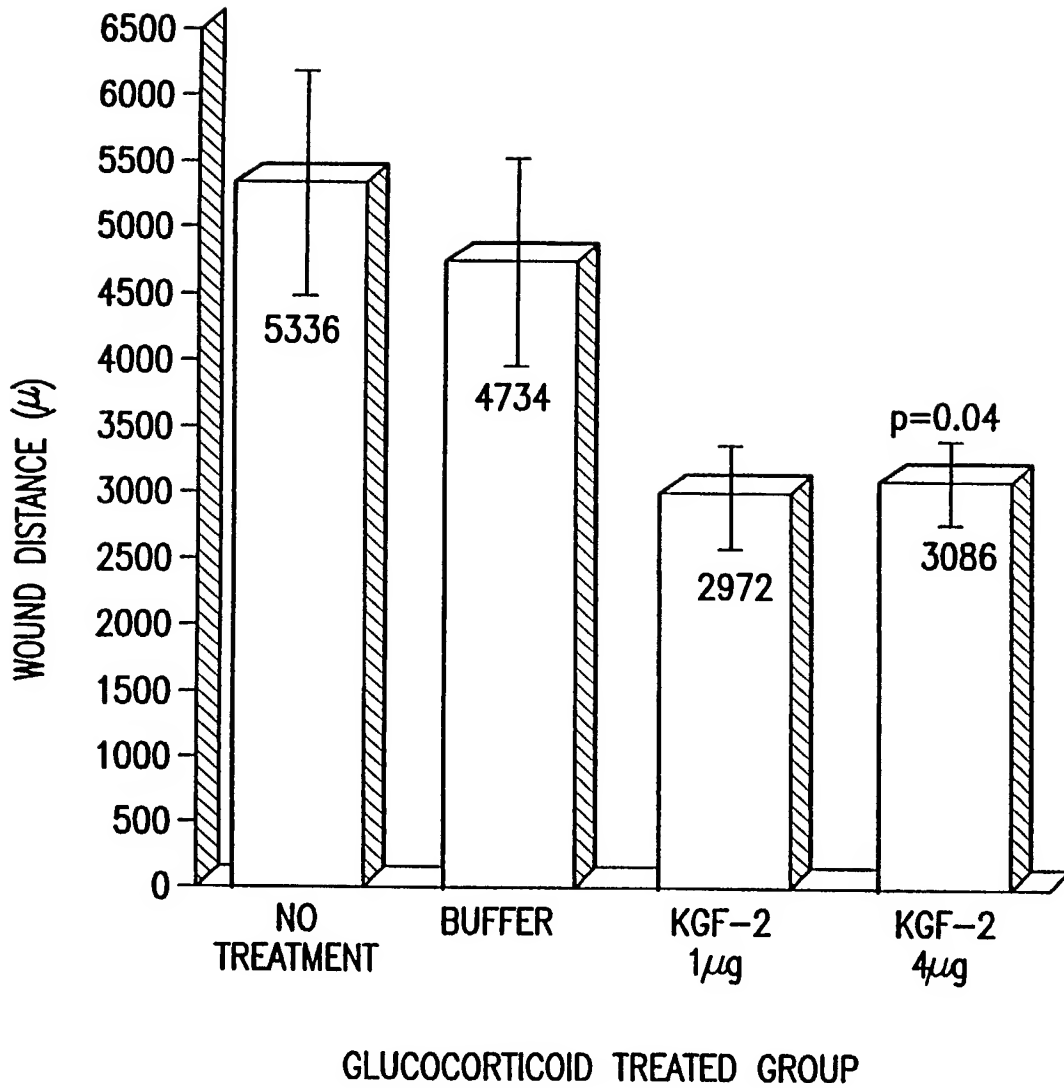


FIG.20

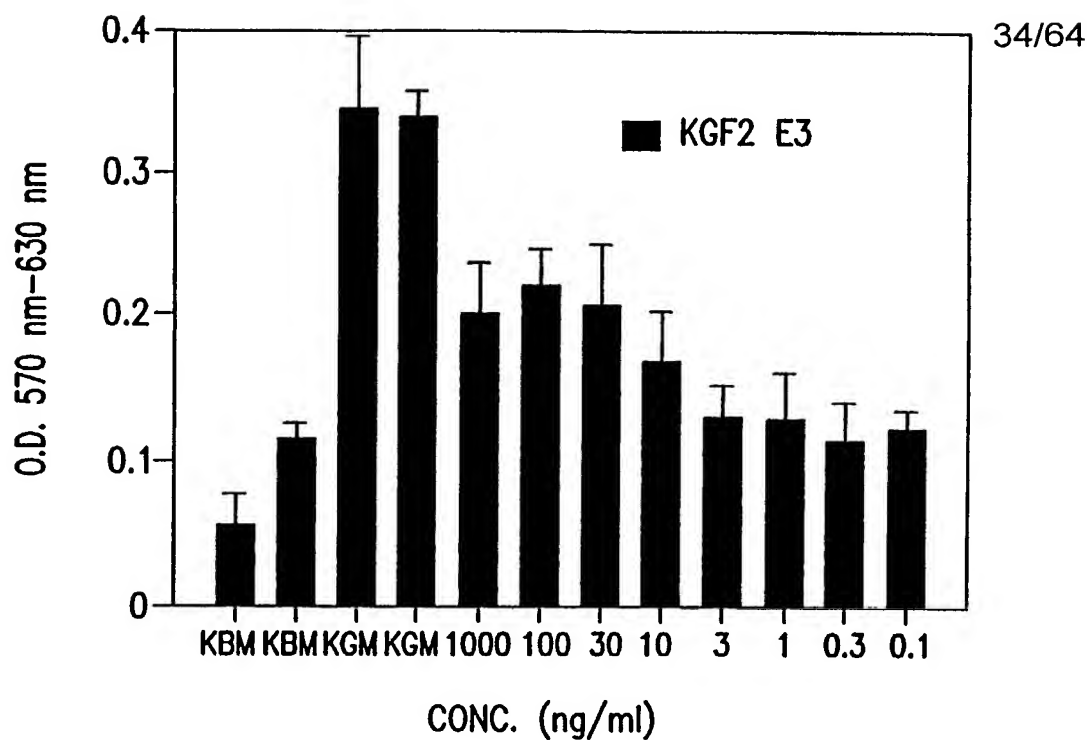


FIG. 21A

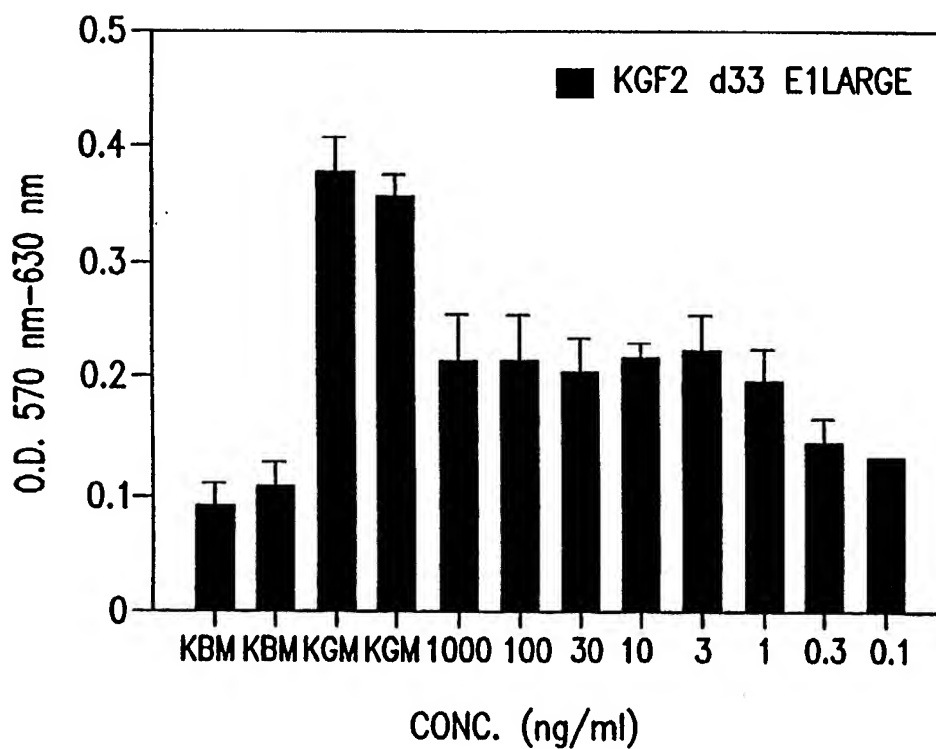


FIG. 21 B



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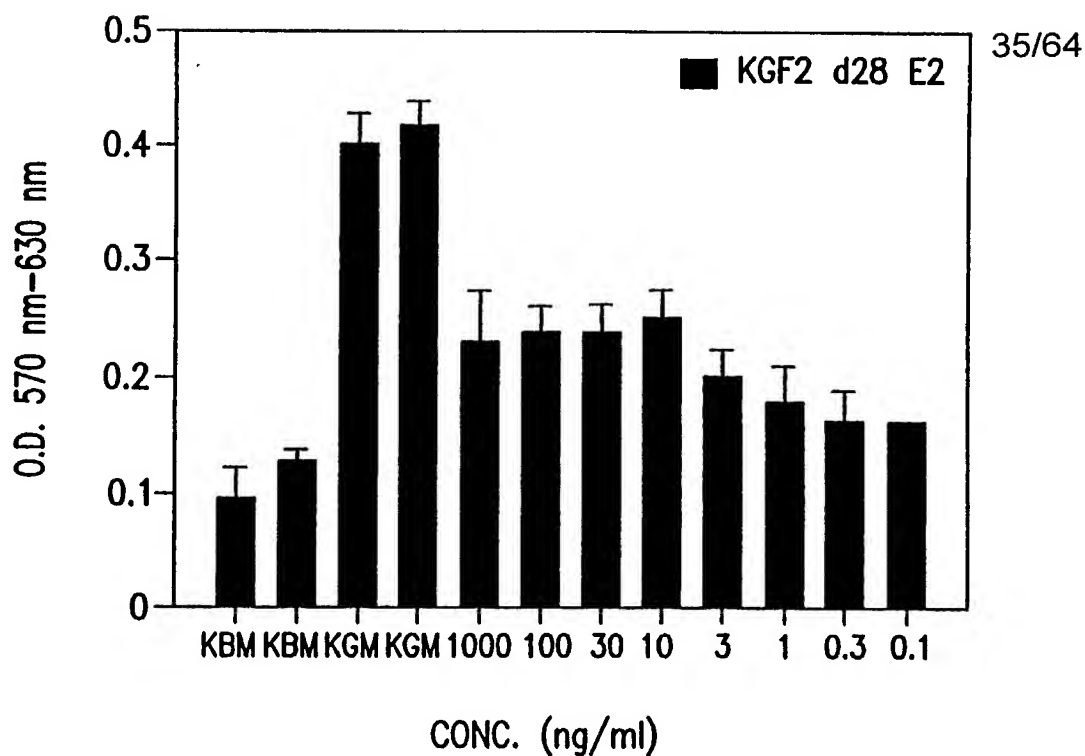


FIG.21C

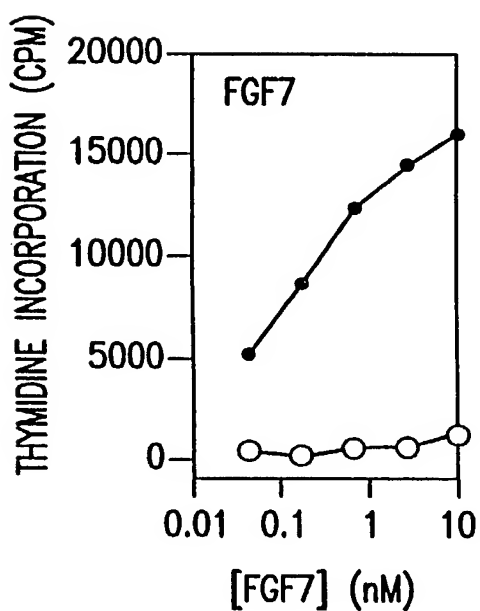


FIG.22A

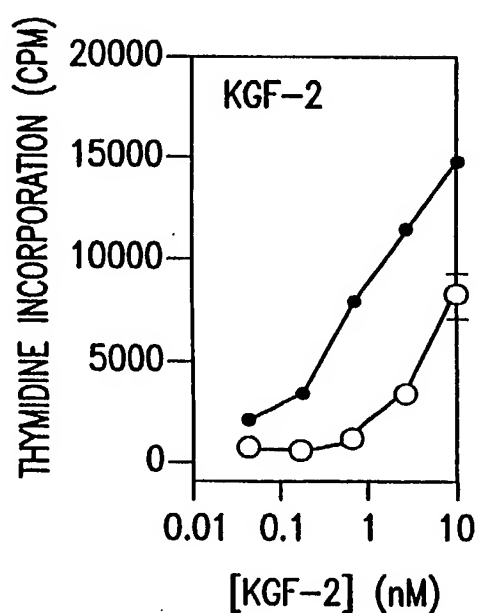


FIG.22A-1



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User: 10/23/2002 10:00:00 AM

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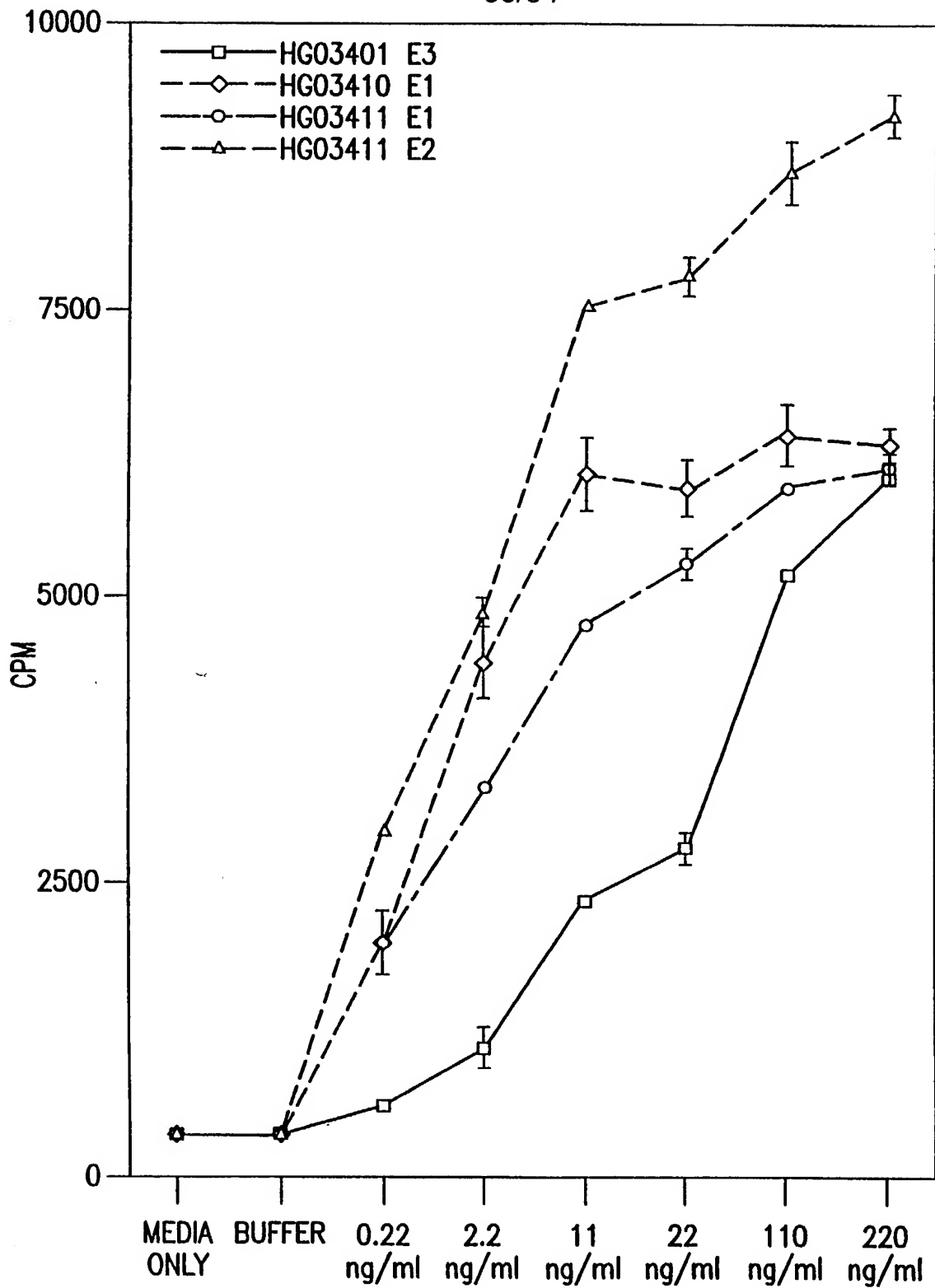


FIG.22B



FIG. 22C is a bar graph showing the results of a competition assay. The y-axis represents CPM (Counts Per Minute) and the x-axis represents the concentration of the competitor (ng/ml). The legend indicates three conditions: 3401-E3 (white bars), DELTA 28-E1 (hatched bars), and DELTA 33-E1 (black bars). The graph shows that the binding of 3401-E3 is significantly inhibited by the addition of DELTA 28-E1 and DELTA 33-E1, with DELTA 33-E1 showing the most potent inhibition.

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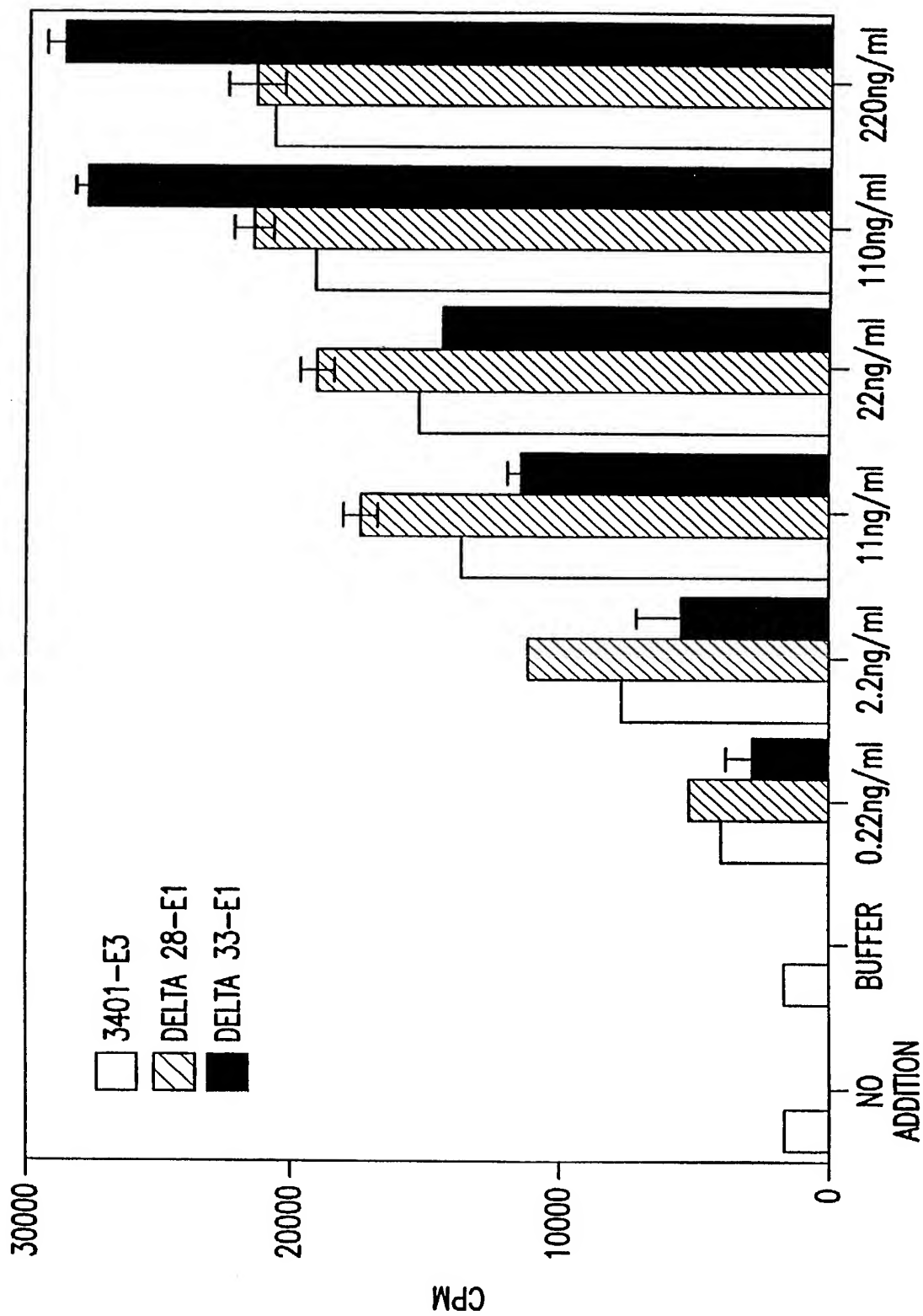


FIG.22C



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ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCT 60
MetThrCysGlnAlaLeuGlyGlnAspMetValSerProGluAlaThrAsnSerSerSer

TCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCTTACAACCACCTGCAG 120
SerSerPheSerSerProSerSerAlaGlyArgHisValArgSerTyrAsnHisLeuGln

GGTGACGTTTCGTTGGCGTAACTGTTCTCTTTACCAAATACTTCCTGAAAATCGAAAA 180
GlyAspValArgTrpArgLysLeuPheSerPheThrLysTyrPheLeuLysIleGluLys

AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACA 240
AsnGlyLysValSerGlyThrLysLysGluAsnCysProTyrSerIleLeuGluIleThr

TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATG 300
SerValGluIleGlyValValAlaValLysAlaIleAsnSerAsnTyrTyrLeuAlaMet

AACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAG 360
AsnLysLysGlyLysLeuTyrGlySerLysGluPheAsnAsnAspCysLysLeuLysGlu

AGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420
ArgIleGluGluAsnGlyTyrAsnThrTyrAlaSerPheAsnTrpGlnHisAsnGlyArg

CAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG 480
GlnMetTyrValAlaLeuAsnGlyLysGlyAlaProArgArgGlyGlnLysThrArgArg

AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG 525
LysAsnThrSerAlaHisPheLeuProMetValValHisSer *

FIG.24A



ATGACTTGCCAGGCACTGGGTCAAGACATGGTTTCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA 40/64
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++| 70
TACTGAACGGTCCGTGACCCAGTTCTGTACCAAGGGCCTTCGATGGTTGTGAGGTGAGATCGAAGT
M T C Q A L G Q D M V S P E A T N S S S S S F
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
GCAGCCCATCTAGCGCAGGTGTCAGTTGCTCTTACAACCACTTACAGGGTGATGTTGCTTGGCGCAA 140
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
CGTCGGGTAGATCGCGTCCAGCAGTCAAGCGAGAATGTTGGTGAATGTCCCACTACAAGCAACCGCGTT
S S P S S A G R H V R S Y N H L Q G D V R W R K
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
ACTGTTCACTTTACCAAGTACTTCTGAAAATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAG 210
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
TGACAAGTCGAAATGGTTCATGAAGGACTTTAGCTTTTTTTGCCATTTCAAAGACCTGGTTCTTCCTC
L F S F T K Y F L K I E K N G K V S G T K K E
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
AACTGCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACA 280
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
TTGACGGGCATGTGCTAGGACCTCTATTGTAGTCATCTTAGCCTCAACAACGGCAGTTTCGGTAATTGT
N C P Y S I L E I T S V E I G V V A V K A I N
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
GCAACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAA 350
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
CGTTGATAATGAATCGGTACTTGTCTTCCCTTTGAGATACGAGTTTCTTAAATTGTTACTGACATT
S N Y Y L A M N K K G K L Y G S K E F N N D C K
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
GCTGAAGGAGAGGATAGAGGAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
CGACTTCCTCTCCTATCTCCTTTTACCTATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCTCC
L K E R I E E N G Y N T Y A S F N W Q H N G R
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
CAAATGTATGTGCATTGAATGAAAAGGAGCTCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCT 490
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
GTTTACATACACGTAACCTTTTCTCGAGGTTCTCTCCTGTCTTTGTGCTTCTTTTGTGGA
Q M Y V A L N G K G A P R R G Q K T R R K N T
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
CTGCTCACTTTCTTCCAATGGTGGTACACTCATAG
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++| 525
GACGAGTGAAAGAAGTTACCACCATGTGAGTATC
S A H F L P M V V H S
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|

FIG.24B



... ..

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ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCTTACAACCAC
CTGCAGGGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAAACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

MTQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVWRKLFSTKYFLKIE
KNGKVSGETTKENCPYSILEITSVEIGVVAVKAINSYYLAMNKKGKLYGSKEFNNDCKL
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVS.

FIG.25

ATGGCTGGTCGTCACGTTCTTACAACCACCTGCAGGGTGACGTTGTTGGCGT
AACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG
GGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATA
GAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAA
ATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAAACGAAGG
AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MAGRIHVRSYNHLQGDVWRKLFSTKYFLKIEKNGKVSGETTKENCPYSILEITSVEIGV
VAVKAINSYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVS.

FIG.26



At the time of filing, the applicant was not aware of the prior art.

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ATGGTTCGTTGGCGTAAACTGTTCTCTTTACCAAATACTTCCTGAAAATCGAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATA
ACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTA
GCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAAGAATTTAACAATGACTGTAAG
CTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTAACTGGCAG
CATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGA
CAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCA
TAG

MVRWRKLFSTKYFLKIEKNGKVSgtkkENCpysILEITSVEIGVVAVKAINSnyyLAM
NKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTR
RKNTSAHFLPMVVHS.

FIG.27

ATGGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCAT
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCA
ACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAAGAATTTAAC
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATC
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCA
ATGGTGGTACACTCATAG

MEKNGKVSgtkkENCpysILEITSVEIGVVAVKAINSnyyLAMNKKGKLYGSKEFNND
KLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH
S.

FIG.28



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ATGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGT
TGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAAC
TCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA
AATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTA
TGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA
ACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MENCPSYLEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGY
NTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.29

ATGGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAACT
CTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAA
ATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA
CACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

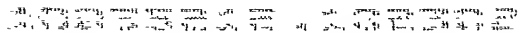
MVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.30

ATGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAG
GATAGAGGAAAATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGA
GGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACA
CGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT
RRKNTSAHFLPMVVHS.

FIG.31



MTCCALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSTKYFLKIE
KNGKVSGETTKENCPSILEITSVEIGVVAVKAINSYYLAMNKKGKLYGSKEFNNDCKL
K

FIG. 32

ATGGCTGGTCGTCACGTTTCGTTCTTACAACCACCTGCAGGGTGACGTTTCGTTGGCGT
AAACTGTTCTCTTTACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG
GGGAAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAG

MAGRHVRSYNHLQGDVWRKLFSTKYFLKIEKNGKVSGTKKENCPSILEITSVEIGV
VAVKAINSNYLAMNKKGKLYGSKEFNNDCKLK

FIG. 33



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C-37 To Ser

ATGACCTCTCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTTCGTTCTTACAACCAC
CTGCAGGGTGACGTTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

FIG.34

C-106 To Ser

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTTCGTTCTTACAACCAC
CTGCAGGGTGACGTTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

FIG.35



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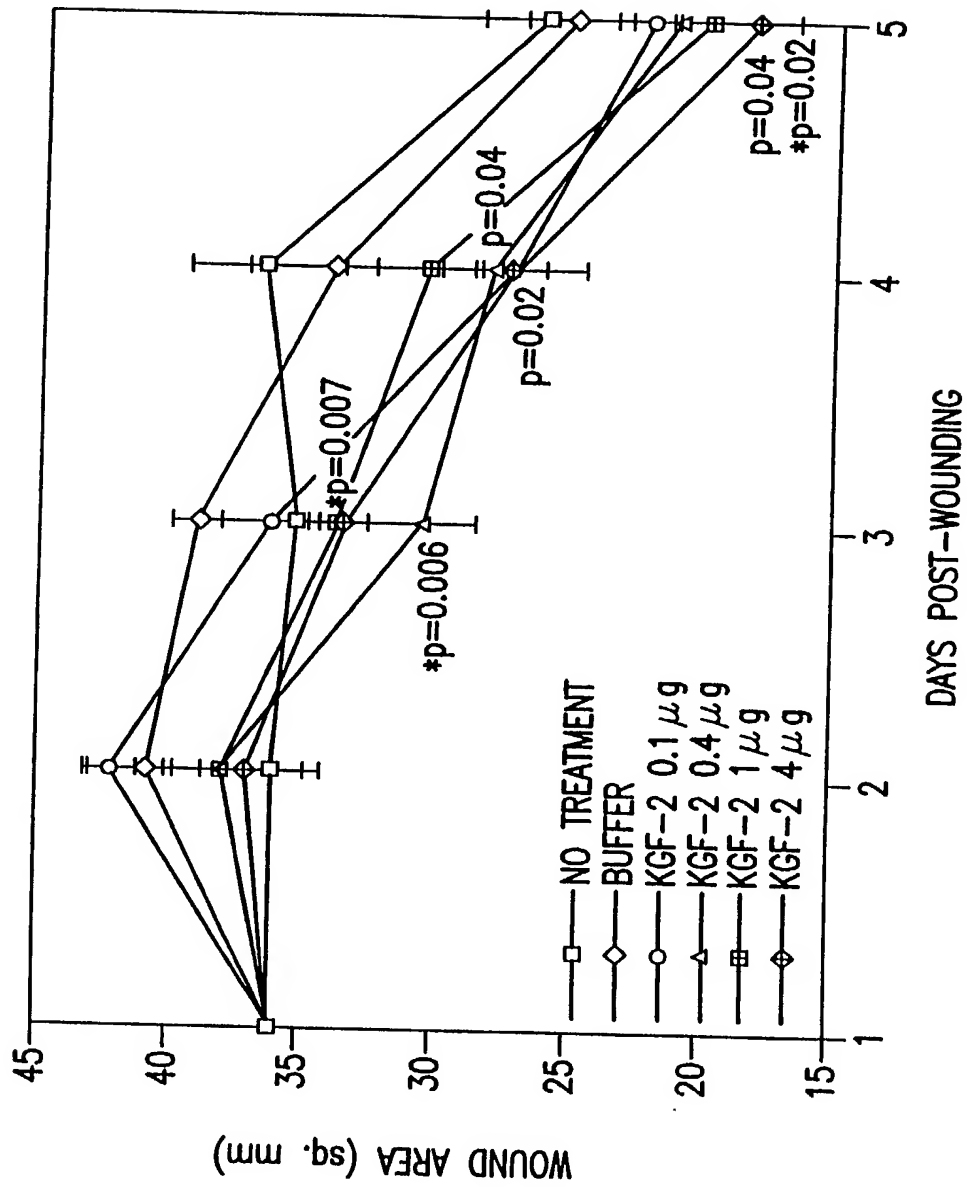


FIG.36



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EFFECT OF KGF-2 $\Delta 33$ ON NORMAL WOUND HEALING RAT MODEL

TREATMENT GROUPS	WOUND SIZE (mm)	% WOUND CLOSURE	HISTOLOGICAL SCORE	RE-EPITH. (μm)	BrdU SCORE
NO TREATMENT	25.9 \pm 2.5	58.8 \pm 3.7	6.8 \pm 0.2	1142 \pm 141	3.8 \pm 0.4
BUFFER	25.1 \pm 1.7	60.2 \pm 2.6	6.4 \pm 0.2	923 \pm 61	5.0 \pm 0.4
KGF-2/ $\Delta 33$ (0.1 μg)	22.0 \pm 0.9	65 \pm 1.4	6.8 \pm 0.2	1275 \pm 148	4.6 \pm 0.7
KGF-2/ $\Delta 33$ (0.4 μg)	21.1 \pm 1.4	68.4 \pm 2.4	8.0 \pm 0.5 p=0.0445*	1310 \pm 182	4.2 \pm 0.7
KGF-2/ $\Delta 33$ (1.0 μg)	19.9 \pm 1.5	66.2 \pm 2.1	8.4 \pm 0.4 p=0.0159* p=0.0053†	1389 \pm 115 p=0.0074†	3.3 \pm 0.25 p=0.0217†
KGF-2/ $\Delta 33$ (4.0 μg)	18.1 \pm 1.6 p=0.0398* p=0.0200†	71.2 \pm 2.6 p=0.0367* p=0.0217†	8.5 \pm 0.3 p=0.0047* p=0.0445†	1220 \pm 89 p=0.0254†	5.3 \pm 0.9

FIG.37



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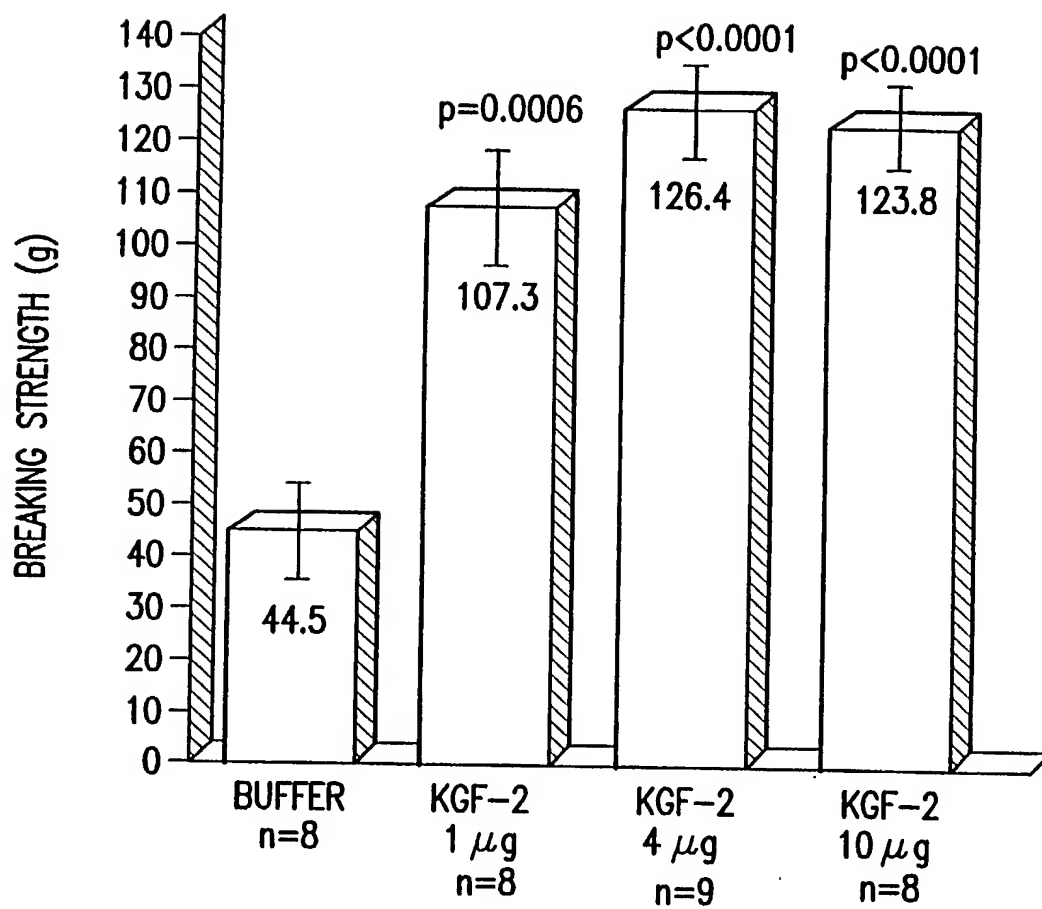


FIG.38



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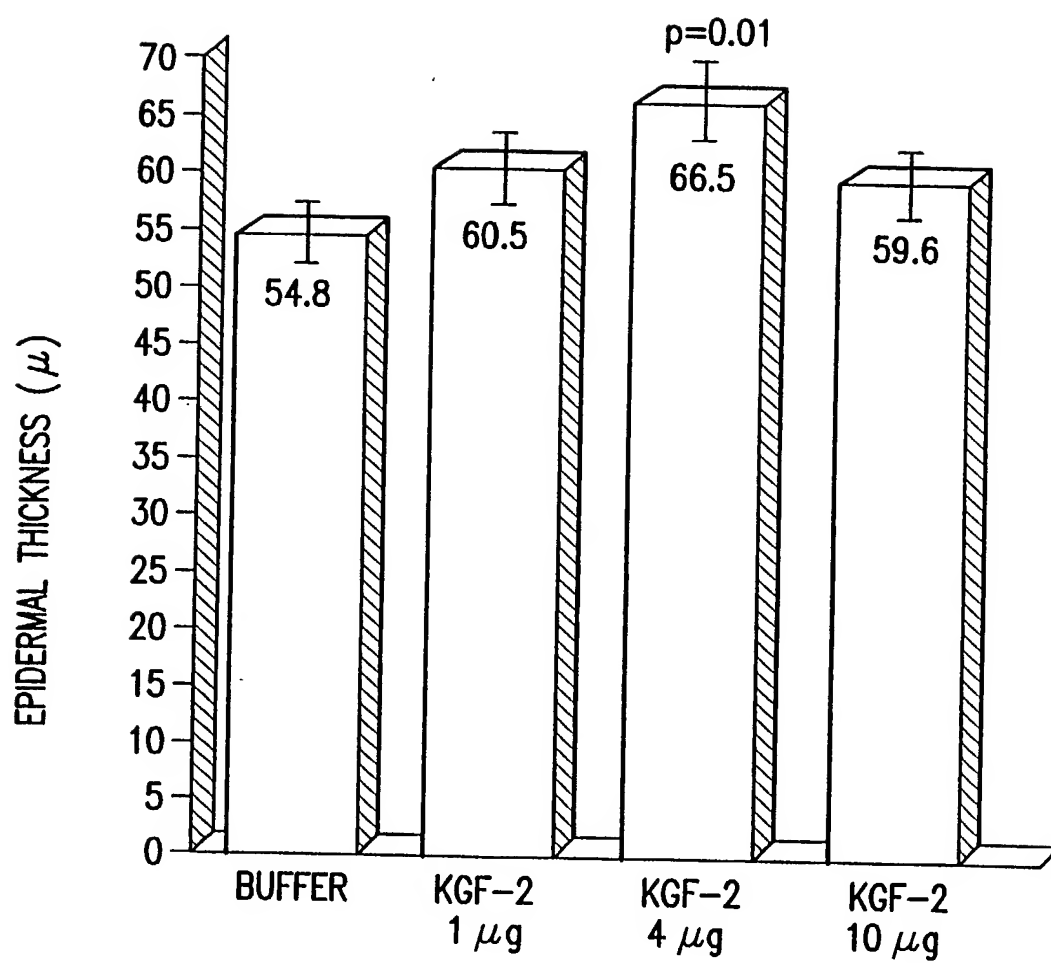


FIG.39



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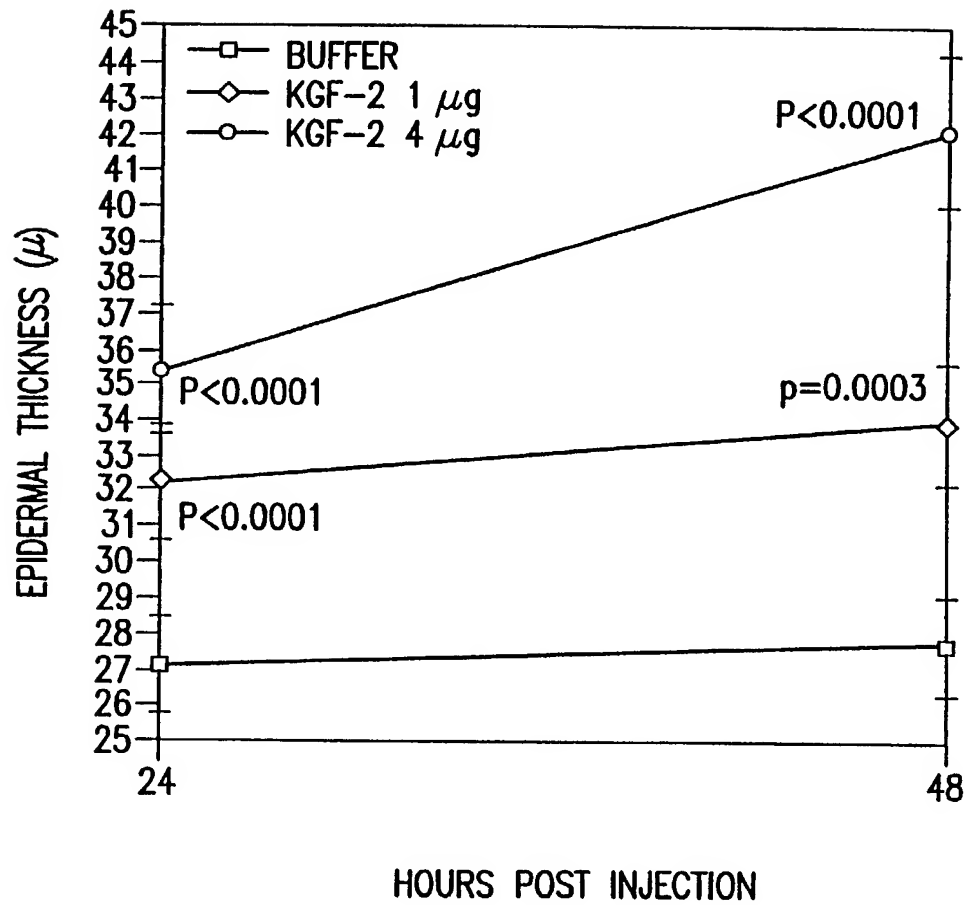


FIG.40



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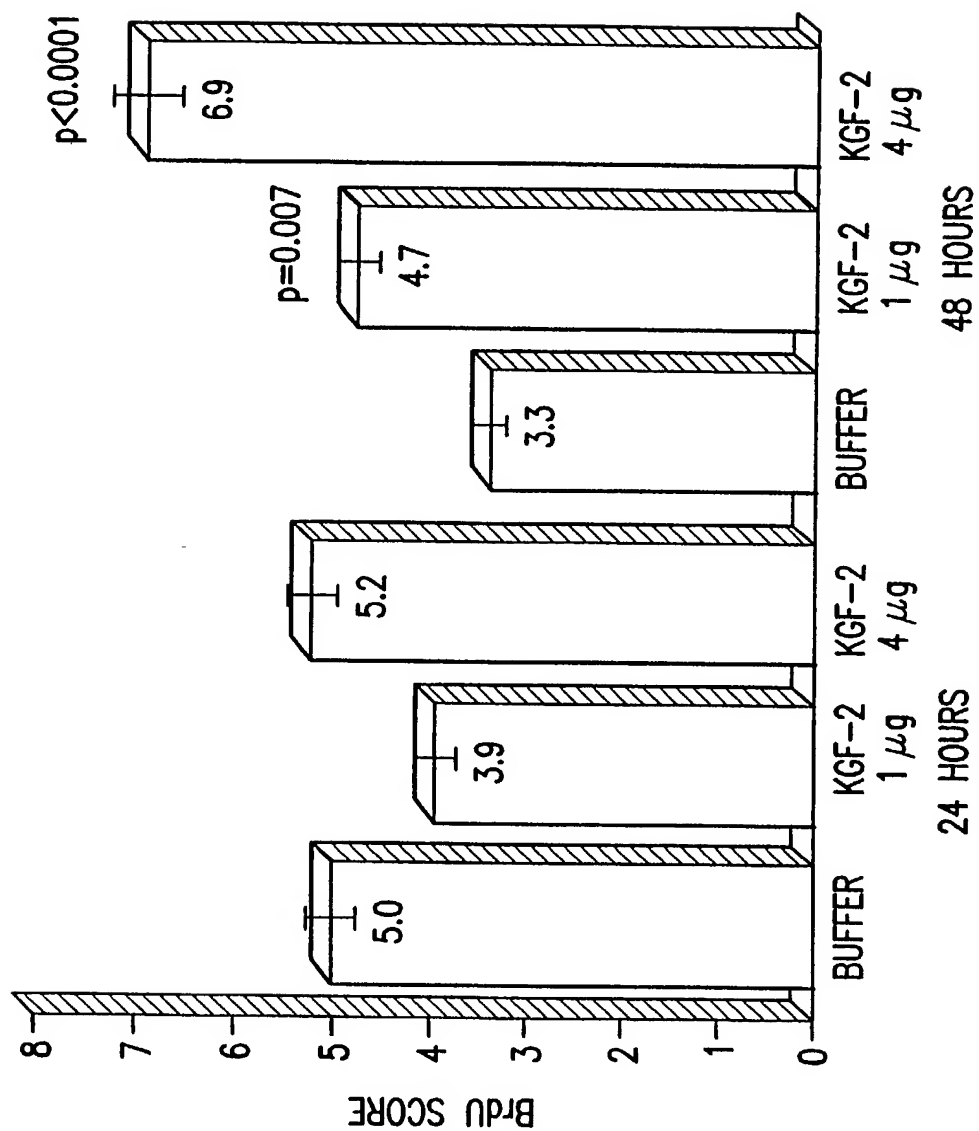


FIG.41

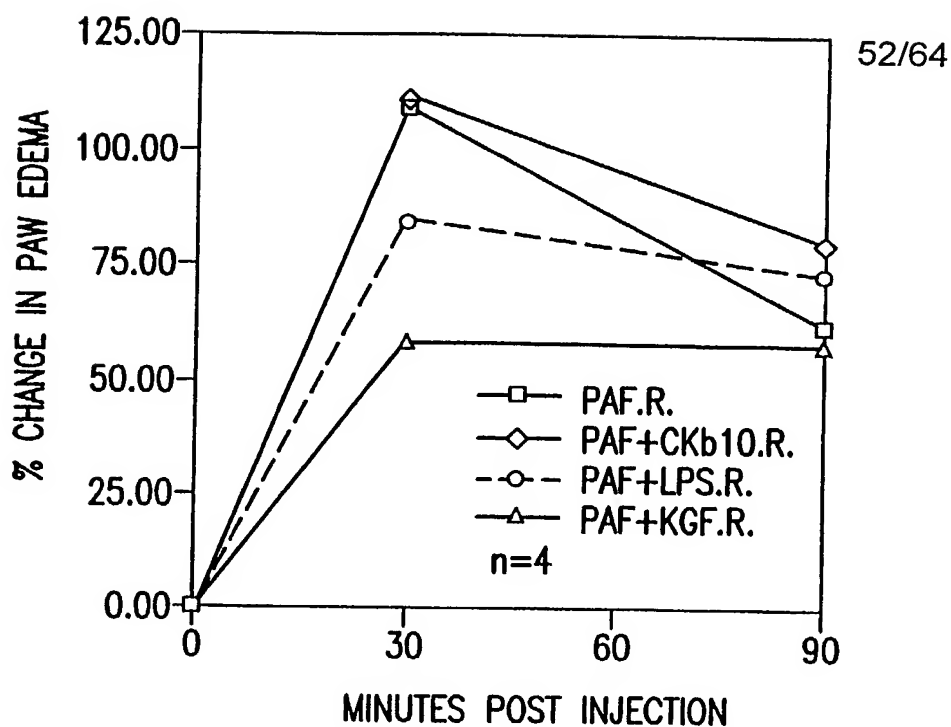


FIG.42A

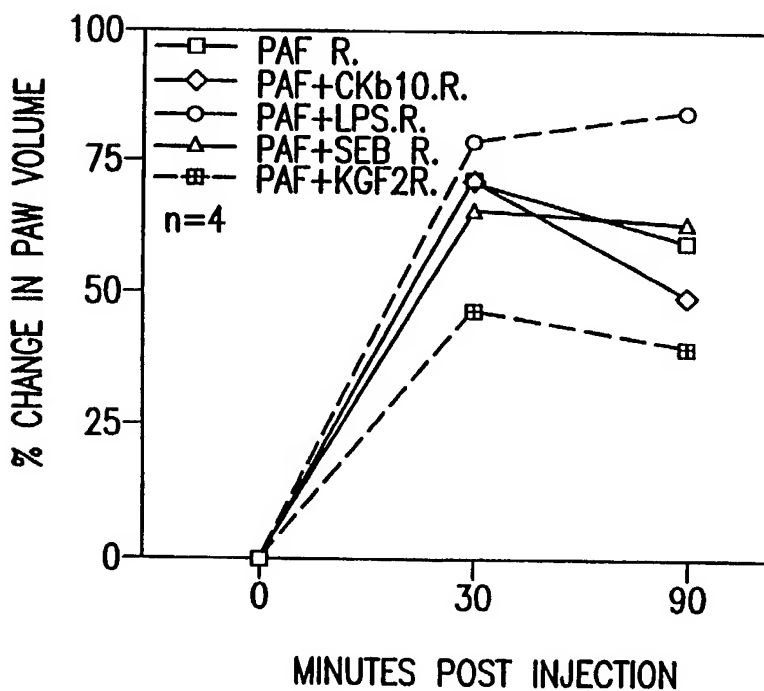


FIG.42B



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EFFECT OF KGF-2 Δ33 ON PAF-INDUCED PAW EDEMA IN LEWIS RATS

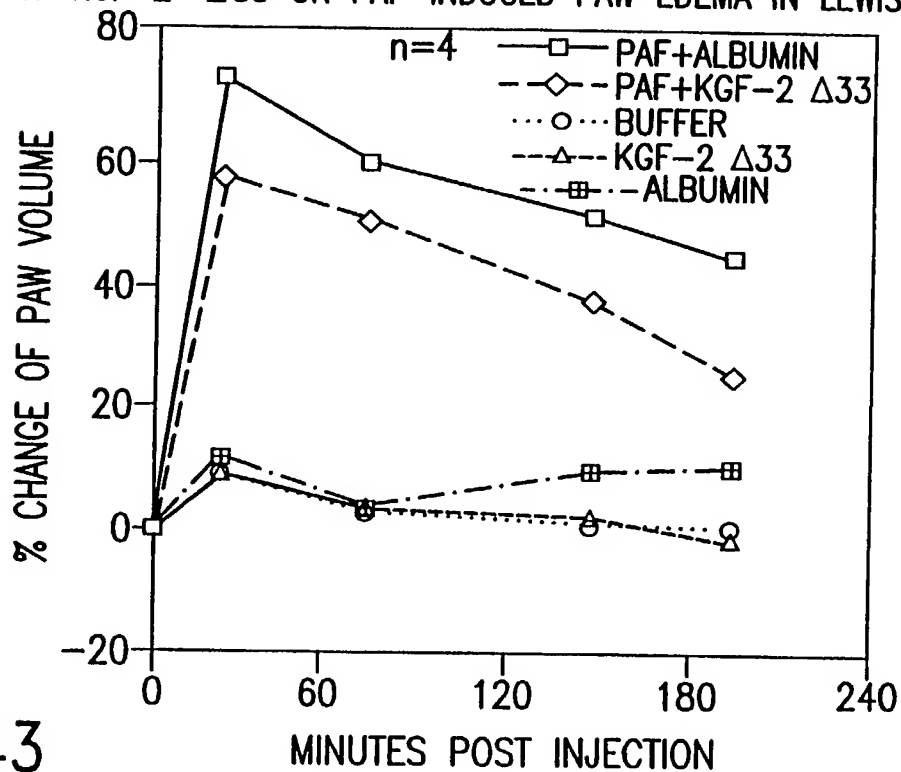


FIG.43

EFFECT OF KGF-2 Δ33 ON SURVIVAL OF WHOLE BODY IRRADIATED Balb/c MICE

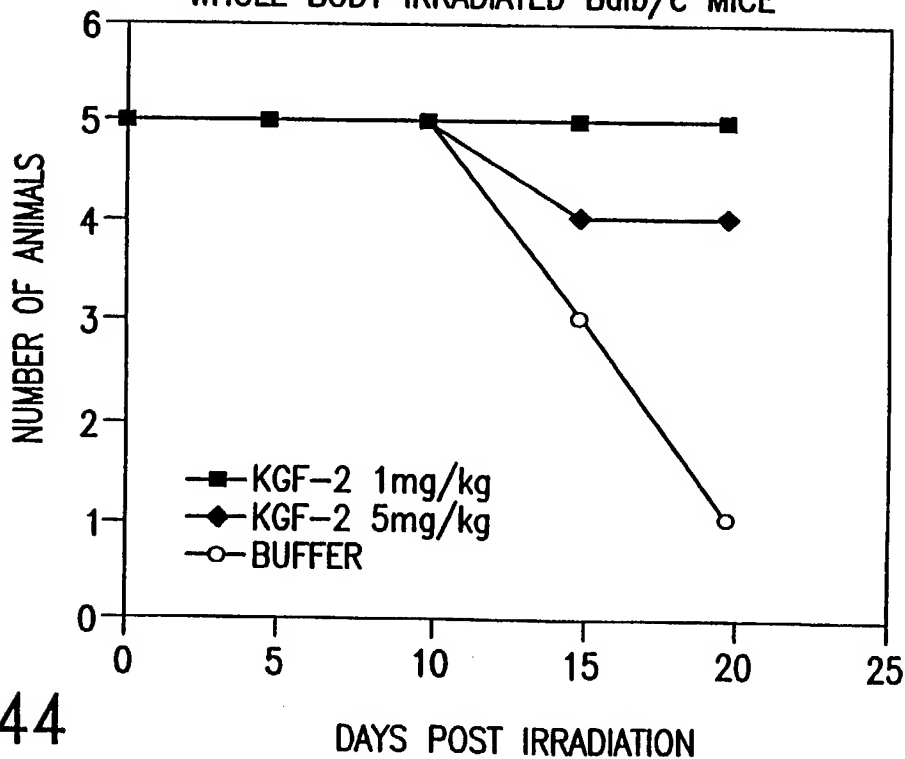


FIG.44



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EFFECT OF KGF-2 Δ 33 ON BODY WEIGHT OF IRRADIATED MICE

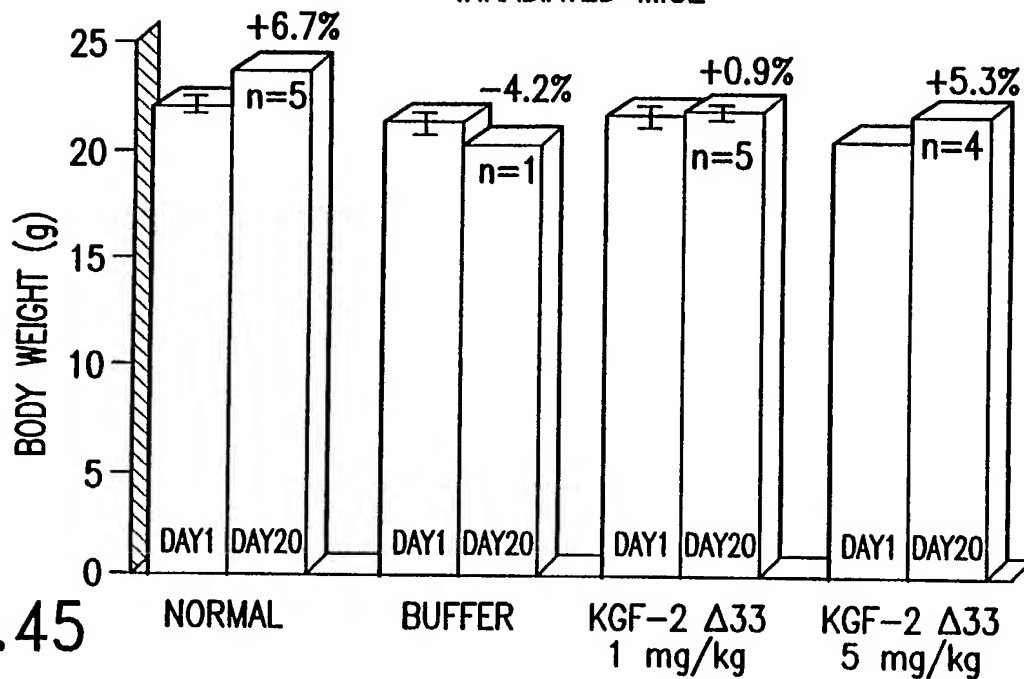


FIG.45

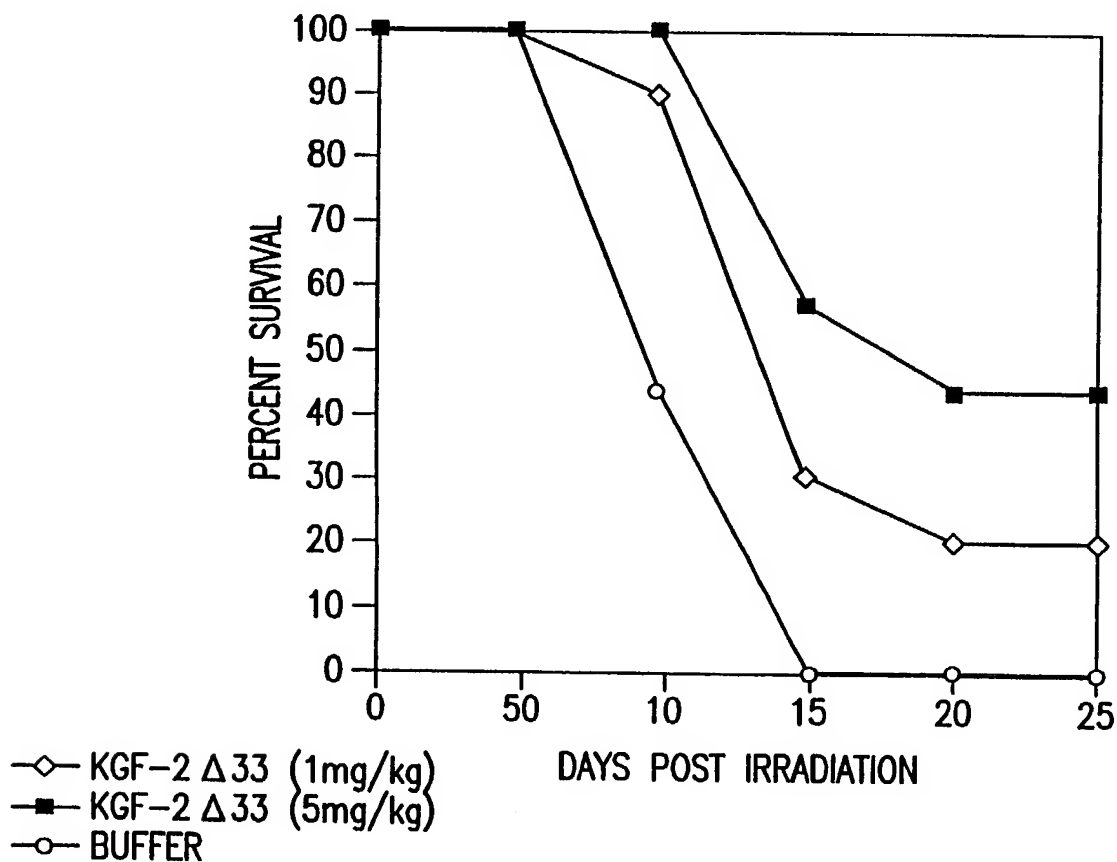


FIG.46



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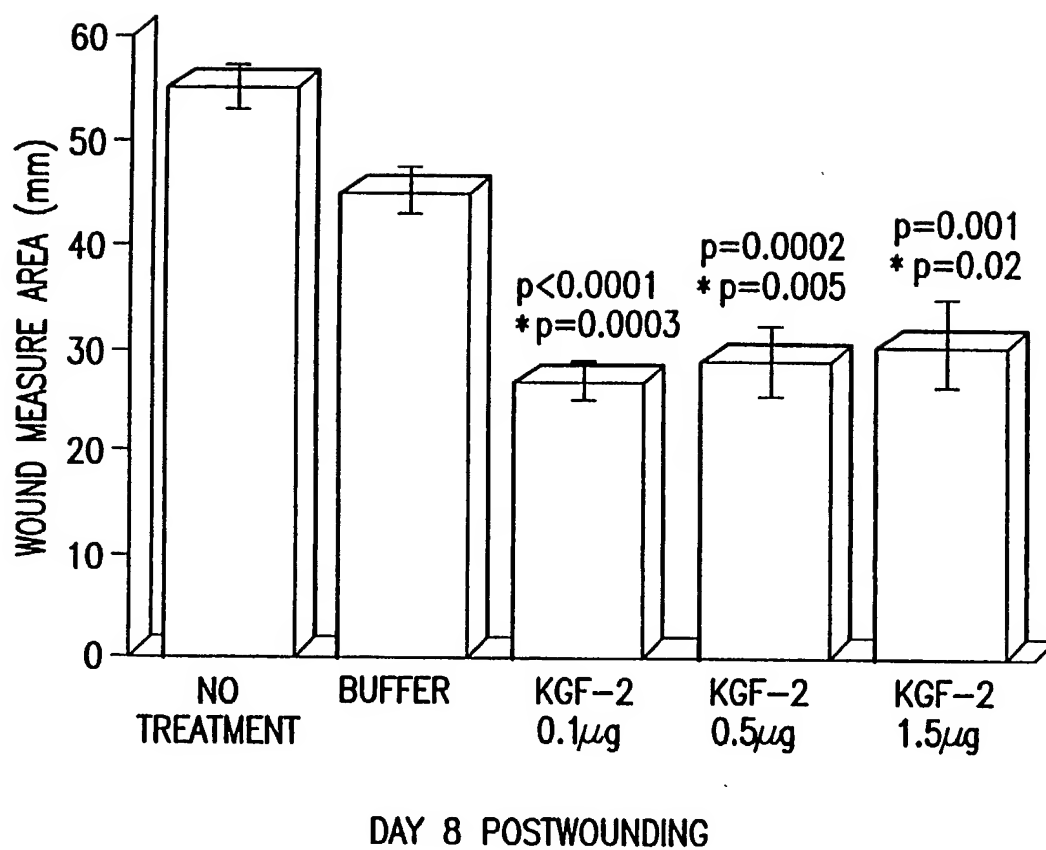


FIG.47



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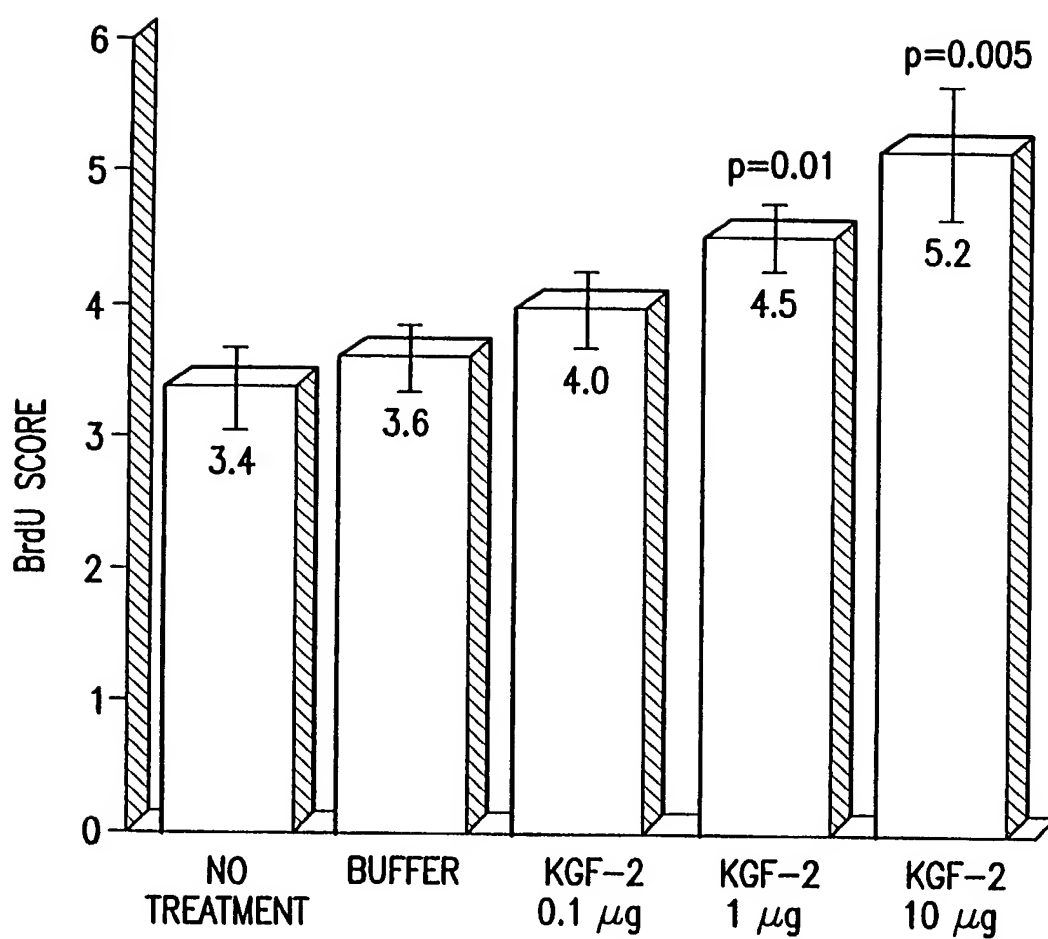


FIG.48



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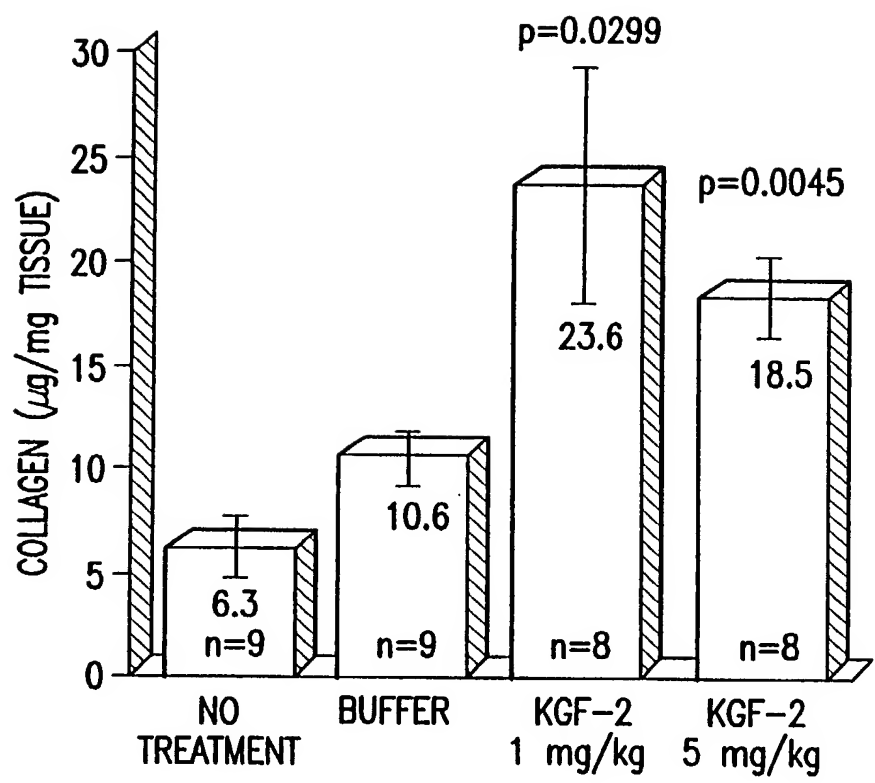


FIG.49



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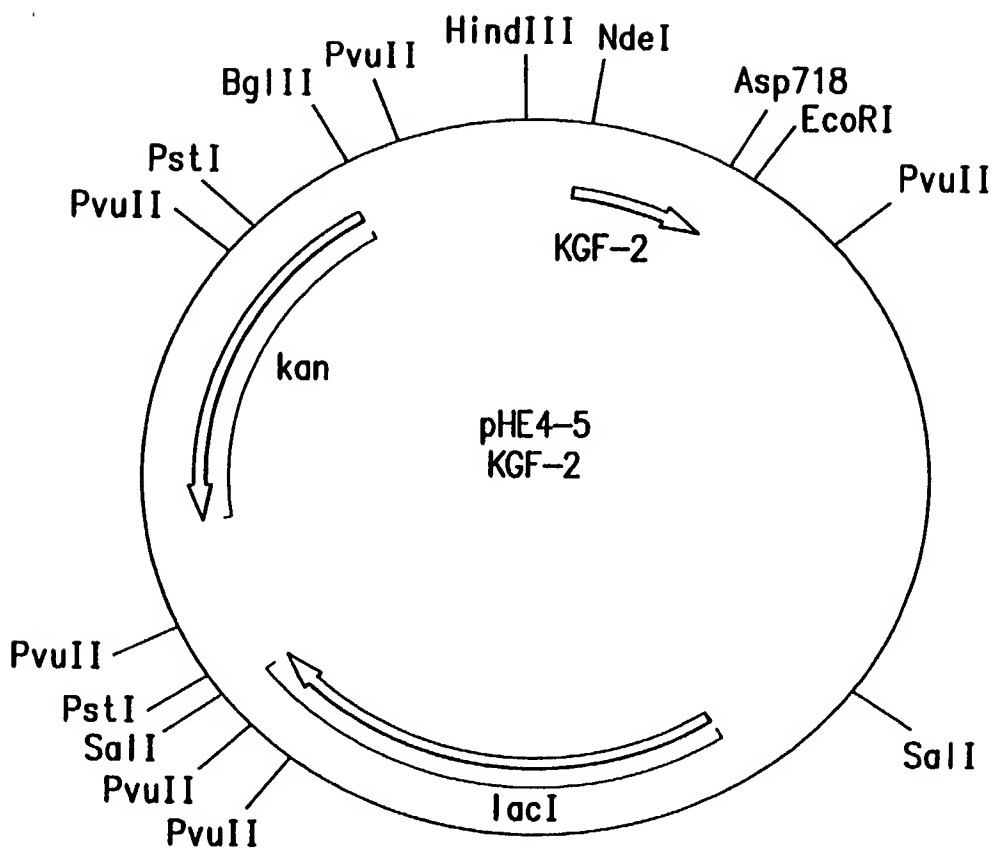


FIG. 50



1 AAGCTTAAAAAACTGCAAAAAATAGT ⁻³⁵ **Operator 1** TTGACTTGTGAGCGGATAACAAT

50 ⁻¹⁰ TAAGATGTACCCA **Operator 2** TTGTGAGCGGATAACAATTTCACACATTAA

94 ^{S/D} AGAGGAGAAATTA CATATG

FIG. 51



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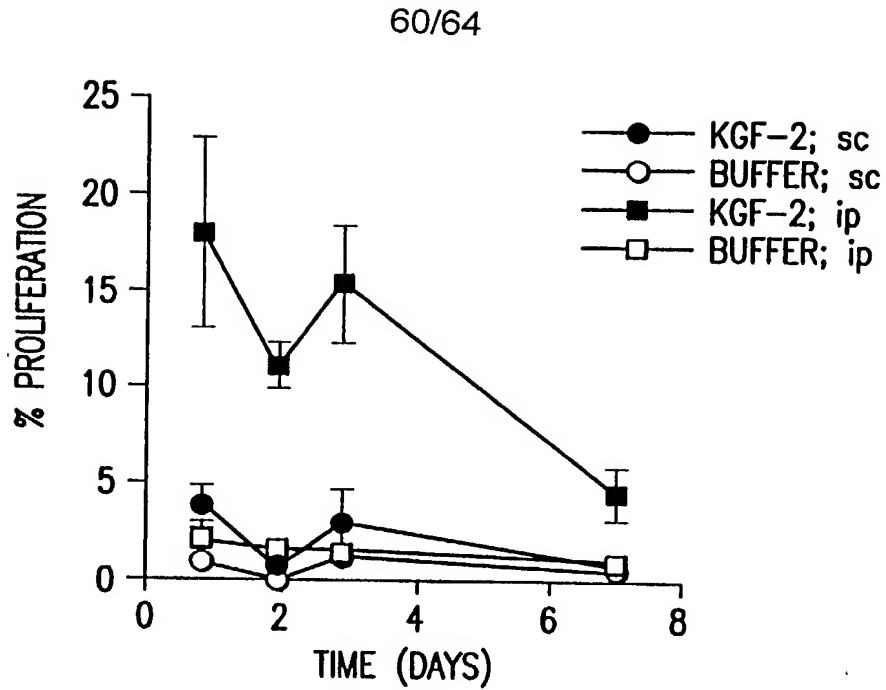


FIG. 52

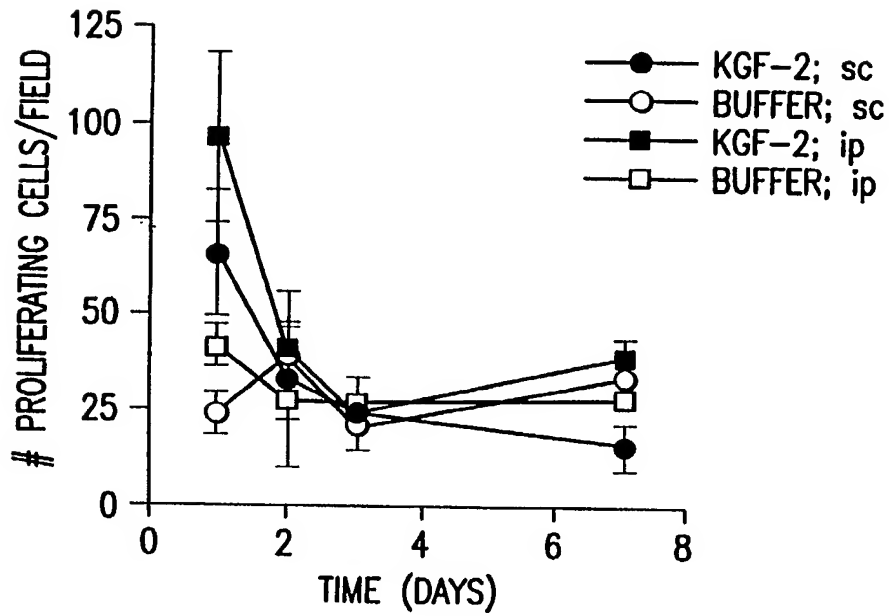
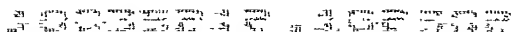


FIG. 53



Group	Percent Ulceration (approx.)	p-value (vs BUFFER)
SALINE CONTROL	1	
BUFFER	37	
KGF-2 1 mg/kg	1	0.0128
KGF-2 5 mg/kg	4	0.0338

Group	Bladder Wall Thickness (approx.)	p-value (vs. Buffer)
SALINE CONTROL	40	
BUFFER	210	
KGF-2 1 mg/kg	100	$p=0.0077$
KGF-2 5 mg/kg	50	$p<0.0001$

FIG. 55



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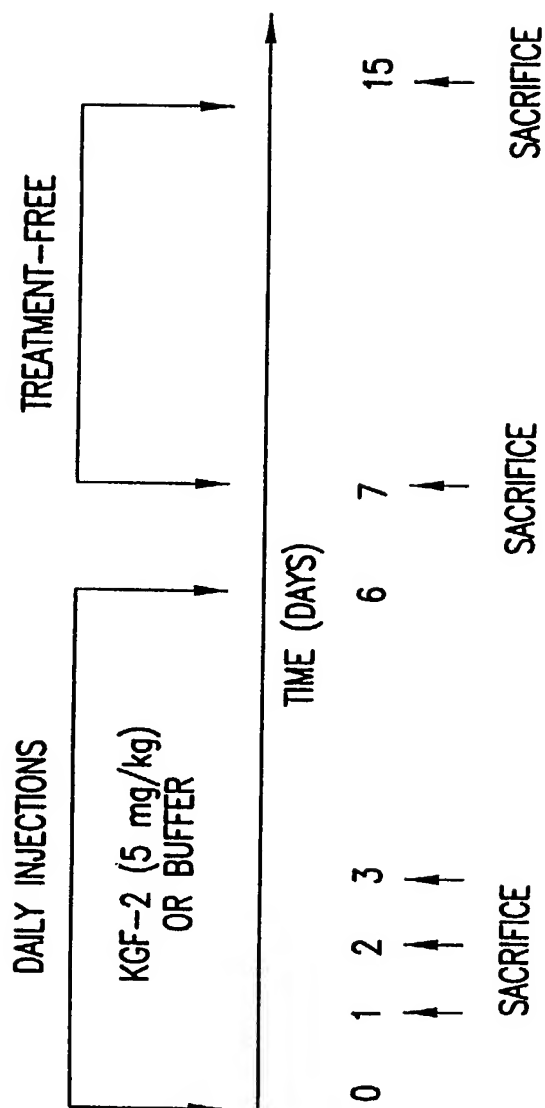


FIG. 56



3,500 7,000 10,000 15,000 20,000

PROLIFERATION OF HEPATOCYTES FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2 63/64

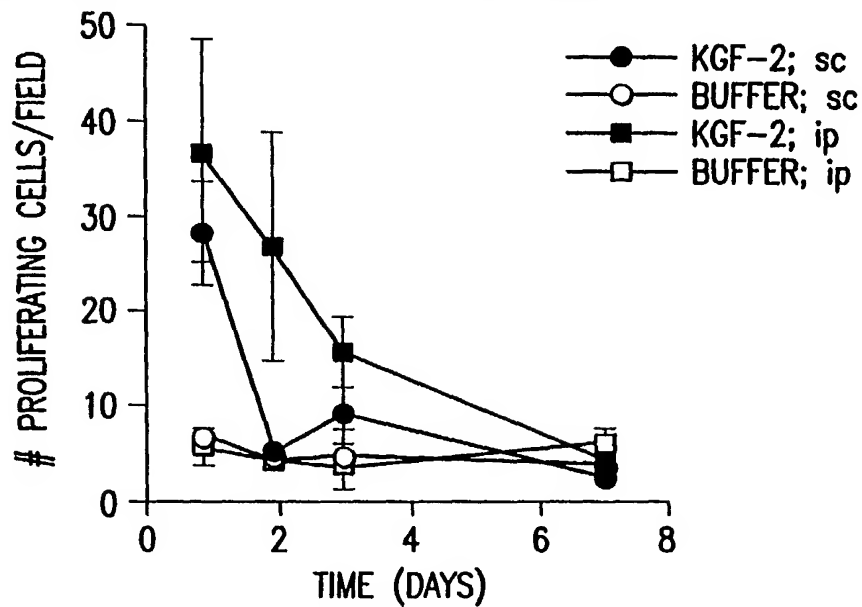


FIG. 57

PROLIFERATION OF PANCREATIC CELLS FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

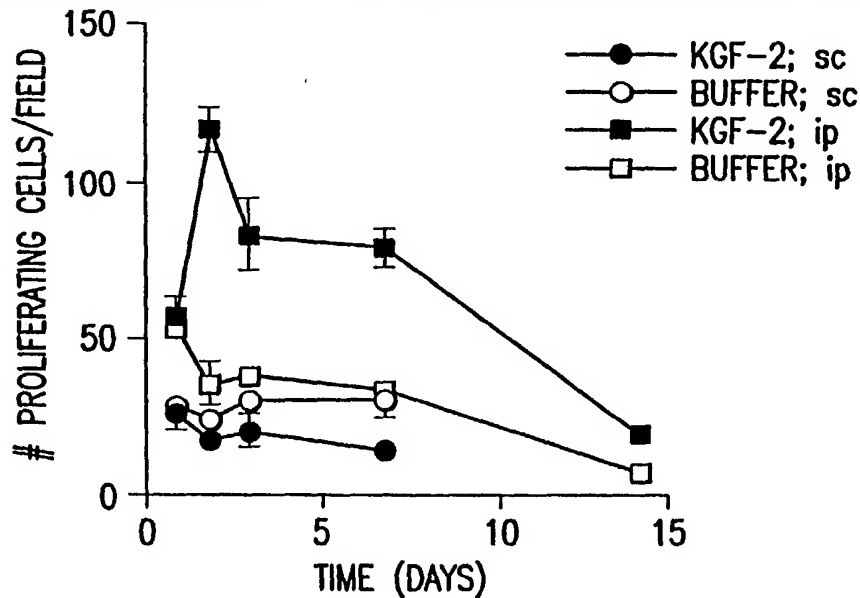


FIG. 58



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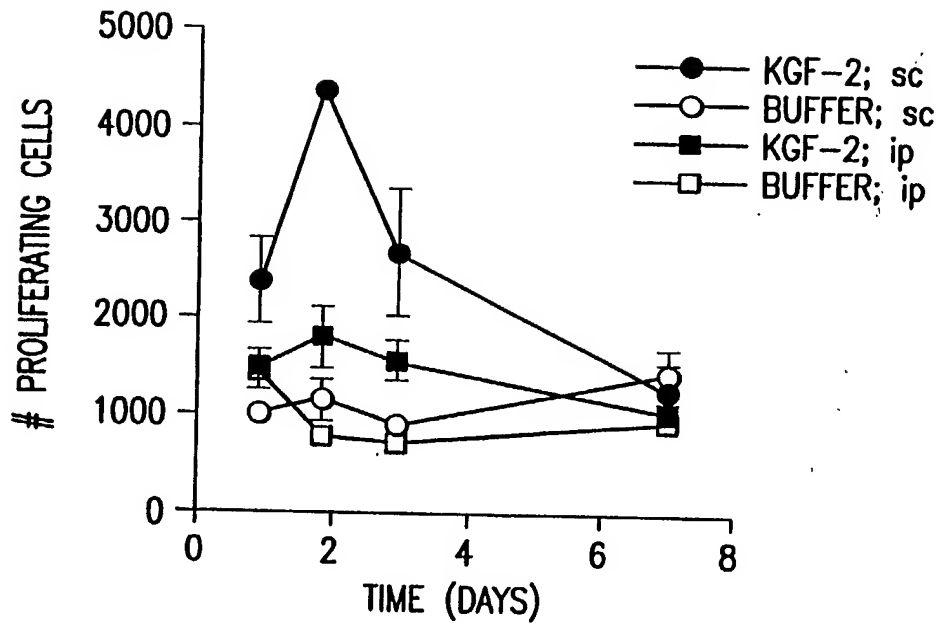


FIG. 59

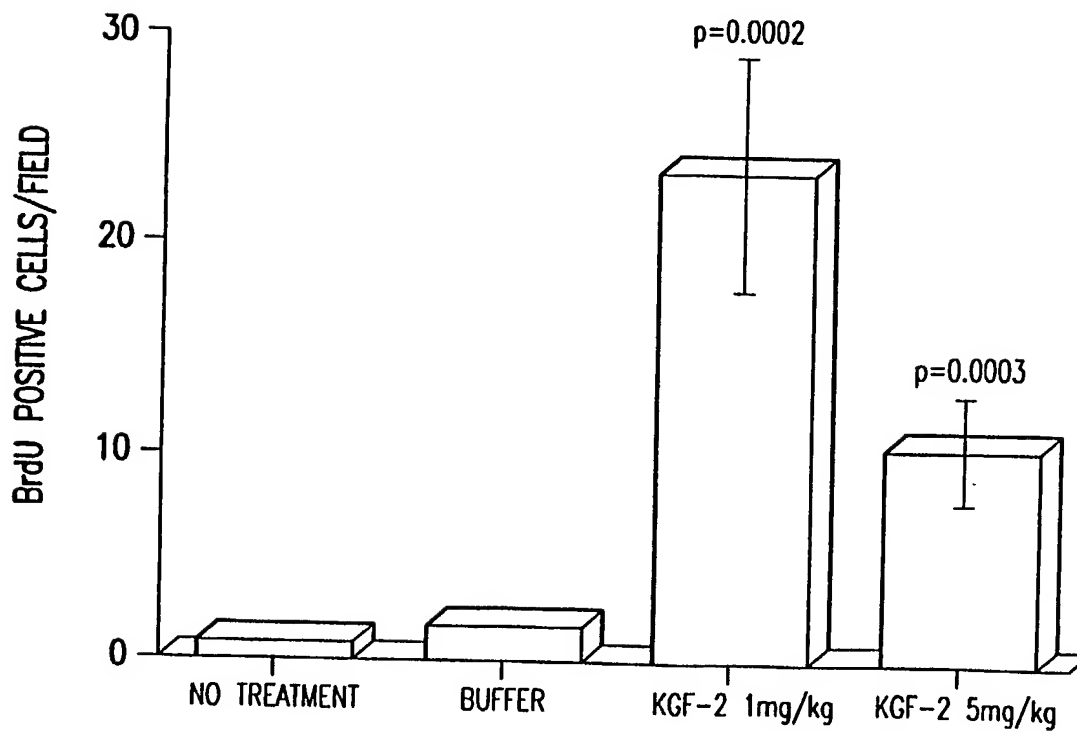


FIG. 60